

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 2002, 13:46:28 ; Search time 71.25 Seconds

(Without alignments)
886,220 Million cell updates/sec

Title: US-09-899-634A-4

Sequence: 1 MALLCFVILCGVADLTRSL.....SRMGAVPVVIPAQSKDGSIV 365

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPTRMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	1728.5	91.1	366	11 Q9DBJ8	Q9dbj8 mus musculu
2	1726	90.9	358	11 Q9R066	Q9r066 ratus norv
3	1657	87.3	319	6 Q9T079	Q9t079 sus scrofa
4	1633	86.0	344	11 Q9R067	Q9r067 ratus norv
5	1629	85.8	344	4 Q9UKV4	Q9ukv4 homo sapien
6	1613	85.0	352	11 Q9IWK6	Q9iwk6 mus musculu
7	1545	81.4	319	6 Q9T080	Q9t080 canis famli
8	1009	53.2	372	13 Q90T50	Q90t50 brachydanio
9	641	33.8	164	11 Q99K60	Q99k60 mus musculu
10	471	24.8	373	4 Q9H6B4	Q9h6b4 homo sapien
11	440.5	23.2	373	11 Q920S5	Q920s5 mus musculu
12	360.5	19.0	394	11 Q925F2	Q925f2 mus musculu
13	336.5	17.7	319	11 Q922D5	Q922d5 mus musculu
14	335.5	17.7	390	6 Q9SK13	Q9sk13 macaca fasc
15	327.5	17.3	304	11 Q9CVA4	Q9cva4 mus musculu
16	326.5	17.2	319	11 Q9JKA5	Q9jka5 mus musculu

17	325.5	17.1	390	4 Q96AP7	Q96ap7 homo sapien
18	323.5	17.0	327	4 Q96I07	Q96i07 homo sapien
19	323.5	17.0	390	4 Q96T50	Q96t50 homo sapien
20	322	17.0	335	13 Q9TGV5	Q9tgv5 gallus gall
21	319.5	16.8	325	4 Q95791	Q95791 homo sapien
22	317	16.7	318	13 Q91664	Q91664 xenopus lae
23	312	16.4	335	13 Q9PWR4	Q9pwr4 gallus gall
24	309.5	16.3	284	4 Q9NXX2	Q9nxx2 homo sapien
25	309	16.3	335	13 Q9YGH1	Q9ygh1 gallus gall
26	306	16.1	328	11 Q92I09	Q92i09 mus musculu
27	290.5	15.3	407	11 Q9D2J4	Q9d2j4 mus musculu
28	284	15.0	248	11 Q9D0T4	Q9d0t4 mus musculu
29	258	13.6	259	4 Q95532	Q95532 homo sapien
30	224	11.8	300	11 Q9D9J0	Q9d9j0 mus musculu
31	223	11.7	300	11 Q9DA22	Q9da22 mus musculu
32	195.5	10.3	181	13 Q91665	Q91665 xenopus lae
33	174.5	9.2	300	11 Q9JHY1	Q9jhy1 ratus norv
34	172	9.1	280	13 Q93716	Q93716 grus americ
35	171.5	9.0	298	11 Q9J159	Q9j159 mus musculu
36	170	9.0	510	11 Q9JLB8	Q9jlb8 mus musculu
37	169.5	8.9	438	11 Q9JLB7	Q9jlb7 mus musculu
38	167	8.8	399	4 Q9Y279	Q9y279 homo sapien
39	166	8.7	259	4 Q9Y532	Q9y532 homo sapien
40	165	8.7	1094	4 Q9BYB8	Q9byb8 homo sapien
41	164.5	8.7	483	4 Q9UF14	Q9uf14 homo sapien
42	164.5	8.7	1093	4 Q96JAL	Q96jal homo sapien
43	162	8.5	740	11 Q9D332	Q9d332 mus musculu
44	161.5	8.5	306	11 Q9RI29	Q9ri29 mus musculu
45	160.5	8.5	310	11 Q9EPK4	Q9epk4 mus musculu

ALIGNMENTS

RESULT	ID	Q9DBJ8	PRELIMINARY;	PRT;	366 AA.
1	Q9DBJ8	Q9DBJ8			
AC	Q9DBJ8	Q9DBJ8			
DT	01-JUN-2001	(TREMURBL_17, Created)			
DT	01-JUN-2001	(TREMURBL_17, Last sequence update)			
DT	01-DEC-2001	(TREMURBL_19, Last annotation update)			
DE	COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.				
GN	CKADR.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=LIVER;				
RX	MEDLINE=21085660; PubMed=11217851;				
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arakawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,				
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,				
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batlov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,				
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,				
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Guernicich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzatelli J., Mombert P.,				
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,				
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,				
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,				
RA	Hayashizaki Y.,				
RT	"Functional annotation of a full-length mouse cDNA collection."				
RL	Nature 409:685-690(2001).				
DR	EMBL; AK004908; BAB33660.1; -				
DR	MED; MGI:1201679; Cxadr.				

DR InterPro: IPR003599; Ig.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00408; Igc2; 2.
DR SMART: SM00410; Ig_Like; 1.
DR Immunoglobulin domain.
SQ SEQUENCE 366 AA; 40078 MW; DIC3CA7163FB231 CRC64;

Query Match 91.1%; Score 1728.5; DB 11; Length 366;
Best Local Similarity 90.2%; Pred. No. 2.9e-145;
Matches 330; Conservative 17; Mismatches 18; Indels 1; Gaps 1;

QY 1 MALLICFVLLCGVADLTSLSTTPEOMTEKAKGETAYLPCFETLGPEDOGPLDIEMILIS 60
DB 1 MARLICFVLLCGIADFTSGLSITTPQRIEKAKGETAYLPCFETLSPEDOGPLDIEMILIS 60
61 PADNOKVDVITLLYSGDKTYDDYODLKGKRVHFTSNLKSQDASINVTNMQLSDIGTYQC 120
DB 61 PSDNQIVDVIITLLYSGDKTYDDYODLKGKRVHFTSNLKSQDASINVTNMQLSDIGTYQC 120
QY 121 KVKKAPGVGNKKIOLTVLLKPSGTRCYVDGSEIGNDFLKCPEKGSLLPLYEMOKLSN 180
DB 121 KVKKAPGVGNKKFLLTVLKPSTGRCFVDSGEISGNDFLKCPEKGSLLPLYEMOKLSN 180
QY 181 SOKLPTLMLAEMTSPIVSYKNASTEYSCTYKKNRVSDDCLRLDVPVPSNRAGTIA 240
DB 181 SOKLPTLMLAEMTSPIVSYKNASTEYSCTYKKNRVSDDCLRLDVPVPSNRAGTIA 240
QY 181 SOKLPTLMLAEMTSPIVSYKNASTEYSCTYKKNRVSDDCLRLDVPVPSNRAGTIA 240
DB 181 SOKLPTLMLAEMTSPIVSYKNASTEYSCTYKKNRVSDDCLRLDVPVPSNRAGTIA 240
QY 241 GAVIGTLLALVLTGILVFCCHKRREKEYEKVHHDIRDVPVPPKSRSTASTASYGSNHS 300
DB 241 GAVIGTLLALVLTGILVFCCHKRREKEYEKVHHDIRDVPVPPKSRSTASTASYGSNHS 300
QY 301 SLGSMSPSMMEGYSKTYNQVPSDEFEERAPQSPPLAKVAAPNLSRMGAVPVMIPAQS 359
DB 301 SLGSMSPSMMEGYSKTYNQVPSDEFEERAPQSPPLAKVAAPNLSRMGAVPVMIPAQS 360
QY 360 KDGSIY 365
DB 361 KDGSIY 366

RESULT 2

Q9R066 PRELIMINARY; PRT; 358 AA.
Q9R066: 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE COXSACKIE-ADENOVIRUS-RECEPTOR HOMOLOG (FRAGMENT).
GN CARL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=LIVER;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultzeis H.-P.,
LA Lamers J.M.J., Poller W.;
RT "Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers";
RL Gene Ther. 6:1520-1535(1999).
DR EMBL, AF109644; AAF01255.1; -
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.

DR Pfam: PF00047; Ig; 2.
DR SMART: SM00408; Igc2; 1.
DR SMART: SM00410; Ig_Like; 1.
DR Immunoglobulin domain; Receptor.
FT NON_TER 358
SQ SEQUENCE 358 AA; 39261 MW; 731B7384A786BB04 CRC64;

Query Match 90.9%; Score 1726; DB 11; Length 358;
Best Local Similarity 91.6%; Pred. No. 4.6e-145;
Matches 328; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLICFVLLCGVADLTSLSTTPEOMTEKAKGETAYLPCFETLGPEDOGPLDIEMILIS 60
DB 1 MARLICFVLLCGVADFTSLSTTPEQRIEKAKGETAYLPCFETLSPEDOGPLDIEMILIS 60
61 PADNOKVDVITLLYSGDKTYDDYODLKGKRVHFTSNLKSQDASINVTNMQLSDIGTYQC 120
QY 61 PSDNQIVDVIITLLYSGDKTYDDYODLKGKRVHFTSNLKSQDASINVTNMQLSDIGTYQC 120
DB 61 PSDNQIVDVIITLLYSGDKTYDDYODLKGKRVHFTSNLKSQDASINVTNMQLSDIGTYQC 120
QY 121 KVKKAPGVGNKKIOLTVLLKPSGTRCYVDGSEIGNDFLKCPEKGSLLPLYEMOKLSN 180
DB 121 KVKKAPGVGNKKFLLTVLKPSTGRCFVDSGEISGNDFLKCPEKGSLLPLYEMOKLSN 180
QY 181 SOKLPTLMLAEMTSPIVSYKNASTEYSCTYKKNRVSDDCLRLDVPVPSNRAGTIA 240
DB 181 SOKLPTLMLAEMTSPIVSYKNASTEYSCTYKKNRVSDDCLRLDVPVPSNRAGTIA 240
QY 241 GAVIGTLLALVLTGILVFCCHKRREKEYEKVHHDIRDVPVPPKSRSTASTASYGSNHS 300
DB 241 GAVIGTLLALVLTGILVFCCHKRREKEYEKVHHDIRDVPVPPKSRSTASTASYGSNHS 300
QY 301 SLGSMSPSMMEGYSKTYNQVPSDEFEERAPQSPPLAKVAAPNLSRMGAVPVMIPAQ 358
DB 301 SLGSMSPSMMEGYSKTYNQVPSDEFEERAPQSPPLAKVAAPNLSRMGAVPVMIPAQ 358

RESULT 3

Q9TU79 PRELIMINARY; PRT; 319 AA.
Q9TU79: 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE COXSACKIE-ADENOVIRUS-RECEPTOR HOMOLOG (FRAGMENT).
GN CAR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultzeis H.-P.,
LA Lamers J.M.J., Poller W.;
RT "Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers";
RL Gene Ther. 6:1520-1535(1999).
DR EMBL, AF109646; AAF01257.1; -
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00408; Igc2; 1.
DR SMART: SM00410; Ig_Like; 1.
KW Immunoglobulin domain; Receptor.
FT NON_TER 319
SQ SEQUENCE 319 AA; 35301 MW; C485555A6C9F1B5B CRC64;

Query Match 87.3%; Score 1657; DB 6; Length 319;
Best Local Similarity 99.7%; Pred. No. 5,3e-139;
Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLSTTTPPEOMTEKAKGETAYLPCRFITLGPEDOGPLDIEMILS 60
DB 1 MALLLRFLVLLCGVADLTRSLSTTTPPEOMTEKAKGETAYLPCRFITLGPEDOGPLDIEMILS 60

QY 61 PADNOKVDVVIILYSGDKIYDDYODLKGVRHFTSNDLKSASINVTNLQJSDIGTYOC 120
DB 61 PADNOKVDVVIILYSGDKIYDDYODLKGVRHFTSNDLKSASINVTNLQJSDIGTYOC 120

QY 121 KYKKAAPGVGNKKIQLTVLLKPSGTRCYVDGSEIGDNDFLKCEPKSGSLPLYEMOKLSN 180
DB 121 KYKKAAPGVGNKKIQLTVLLKPSGTRCYVDGSEIGDNDFLKCEPKSGSLPLYEMOKLSN 180

QY 181 SOKLPTLWLAEMTSPVTSVKNASTEYSGTYSCTVKNRVSSDCLRLDVVPPSNRAGTTA 240
DB 181 SOKLPTLWLAEMTSPVTSVKNASTEYSGTYSCTVKNRVSSDCLRLDVVPPSNRAGTTA 240

QY 241 GAVIGVLLALVILGIVFCCHKRREREKEVEVHHDIRDVPPEPKSRSTARSYLSGNS 300
DB 241 GAVIGVLLALVILGIVFCCHKRREREKEVEVHHDIRDVPPEPKSRSTARSYLSGNS 300

QY 301 SLGSMSPSNMEGSKTYQYN 319
DB 301 SLGSMSPSNMEGSKTYQYN 319

RESULT 4
Q9R067 PRELIMINARY; PRT; 344 AA.
ID Q9R067;
AC - Q9R067;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE COXSACKIE-ADENOVIRUS-RECEPTOR HOMOLOG (FRAGMENT).
GN - CAR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISTAR; TISSUE=LIVER;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang X., Eizema K., Pauschinger M.,
Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultzeis H.-P.,
Lamers J.M.J., Poller W.;
RT "Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does
not correlate with adenovector targeting in vivo indicating anatomical
vector barriers";
RT Gene Ther. 6:1520-1535(1999).
DR EMBL, AF109643; AAF01254.1; -.
DR InterPro; IPR003598; I9_C2.
DR InterPro; IPR003600; I9_Like.
DR Pfam; PF00047; I9_2.
DR SMART; SM00408; IGC2.1.
DR SMART; SM00410; IGLike; 1.
KW Immunoglobulin domain; Receptor.
FT NON_TER 344
FT SEQUENCE 344 AA; 38030 MW; DA36498820DBB9B7 CRC64;

Query Match 86.0%; Score 1633; DB 11; Length 344;
Best Local Similarity 91.2%; Pred. No. 8e-137;
Matches 309; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLSTTTPPEOMTEKAKGETAYLPCRFITLGPEDOGPLDIEMILS 60
DB 1 MALLLCFVLLCGVADLTRSLSTTTPPEOMTEKAKGETAYLPCRFITLGPEDOGPLDIEMILS 60

QY 61 PADNOKVDVVIILYSGDKIYDDYODLKGVRHFTSNDLKSASINVTNLQJSDIGTYOC 120
DB 61 PADNOKVDVVIILYSGDKIYDDYODLKGVRHFTSNDLKSASINVTNLQJSDIGTYOC 120

QY 121 KYKKAAPGVGNKKIQLTVLLKPSGTRCYVDGSEIGDNDFLKCEPKSGSLPLYEMOKLSN 180
DB 121 KYKKAAPGVGNKKIQLTVLLKPSGTRCYVDGSEIGDNDFLKCEPKSGSLPLYEMOKLSN 180

QY 181 SOKLPTLWLAEMTSPVTSVKNASTEYSGTYSCTVKNRVSSDCLRLDVVPPSNRAGTTA 240
DB 181 SOKLPTLWLAEMTSPVTSVKNASTEYSGTYSCTVKNRVSSDCLRLDVVPPSNRAGTTA 240

QY 241 GAVIGVLLALVILGIVFCCHKRREREKEVEVHHDIRDVPPEPKSRSTARSYLSGNS 300
DB 241 GAVIGVLLALVILGIVFCCHKRREREKEVEVHHDIRDVPPEPKSRSTARSYLSGNS 300

QY 301 SLGSMSPSNMEGSKTYQYNQVPSDEPERAPQSEFTLPAK 339
DB 301 SLGSMSPSNMEGSKTYQYNQVPSDEPERAPQSEFTLPAK 339

RESULT 5
Q9UKV4 PRELIMINARY; PRT; 344 AA.
ID Q9UKV4;
AC Q9UKV4;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE COXSACKIE AND ADENOVIRUS RECEPTOR PROTEIN (FRAGMENT).
GN HCAR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang X., Eizema K., Pauschinger M.,
Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultzeis H.-P.,
Lamers J.M.J., Poller W.;
RT "Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does
not correlate with adenovector targeting in vivo indicating anatomical
vector barriers";
RT Gene Ther. 6:1520-1535(1999).
DR EMBL, AF124598; AAD31772.1; -.
DR InterPro; IPR003598; I9_C2.
DR InterPro; IPR003600; I9_Like.
DR Pfam; PF00047; I9_2.
DR SMART; SM00408; IGC2.1.
DR SMART; SM00410; IGLike; 1.
KW Immunoglobulin domain; Receptor.
FT NON_TER 344
FT SEQUENCE 344 AA; 38097 MW; EEF372296C697AA CRC64;

Query Match 85.8%; Score 1629; DB 4; Length 344;
Best Local Similarity 90.3%; Pred. No. 1.8e-136;
Matches 306; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLSTTTPPEOMTEKAKGETAYLPCRFITLGPEDOGPLDIEMILS 60
DB 1 MALLLCFVLLCGVADLTRSLSTTTPPEOMTEKAKGETAYLPCRFITLGPEDOGPLDIEMILS 60

QY 61 PADNOKVDVVIILYSGDKIYDDYODLKGVRHFTSNDLKSASINVTNLQJSDIGTYOC 120
DB 61 PADNOKVDVVIILYSGDKIYDDYODLKGVRHFTSNDLKSASINVTNLQJSDIGTYOC 120

QY 121 KYKKAAPGVGNKKIQLTVLLKPSGTRCYVDGSEIGDNDFLKCEPKSGSLPLYEMOKLSN 180
DB 121 KYKKAAPGVGNKKIQLTVLLKPSGTRCYVDGSEIGDNDFLKCEPKSGSLPLYEMOKLSN 180

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OY 181 SOKLPTLWLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 SOKMPTSWLAEMTSSVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
OY 241 GAVIGVLLALVILGIVFCCHKKRREKEYEKEVHHDIREDVPPKRSRTSTARSYLSGNS 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 GAVIGVLLALVILGIVFCCHKKRREKEYEKEVHHDIREDVPPKRSRTSTARSYLSGNS 300
OY 301 SLGSMSPSNMEGYSKTOYNQVNPSEDFERAPQSPPTLPK 339
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 SLGSMSPSNMEGYSKTOYNQVNPSEDFERAPQSPPTLPK 339

RESULT 6
OY1W66 PRELIMINARY: PRT: 352 AA.
ID OY1W66
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
OC COSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCF-2001) to the EMBL/Genbank/DBJ databases.
KW Receptor.
SQ SEQUENCE 352 AA; 38843 MW; 2BD8CBD25D8CE123 CRC64;

Query Match 85.0%; Score 1613; DB 11; Length 352;
Best Local Similarity 89.7%; Pred. No. 5e-135;
Matches 304; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

OY 1 MALLCFVLLCGVADITRSLSTTPPEOMTEKAGETAYLPCTRFLGPEDOGPIIDIEMLLS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MALLCFVLLCGVADITRSLSTTPPEOMTEKAGETAYLPCTRFLGPEDOGPIIDIEMLLS 60
OY 61 PADNOKVQDVIIILYSGDKIYDDYODLKGKRVHTSNDLKSAGASINVTNLQSLDICTYOC 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PADNOKVQDVIIILYSGDKIYDDYODLKGKRVHTSNDLKSAGASINVTNLQSLDICTYOC 120
OY 121 KYKAPGVGNKKIQLTVLKPSTRCYVDGSEIEGDFKLCPEKGSPLYLEMOKLSN 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 KYKAPGVGNKKIQLTVLKPSTRCYVDGSEIEGDFKLCPEKGSPLYLEMOKLSN 180
OY 121 KYKAPGVGNKKIQLTVLKPSTRCYVDGSEIEGDFKLCPEKGSPLYLEMOKLSN 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 KYKAPGVGNKKIQLTVLKPSTRCYVDGSEIEGDFKLCPEKGSPLYLEMOKLSN 180
OY 181 SOKLPTLWLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 SOKMPTSWLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
OY 241 GAVIGVLLALVILGIVFCCHKKRREKEYEKEVHHDIREDVPPKRSRTSTARSYLSGNS 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 GAVIGVLLALVILGIVFCCHKKRREKEYEKEVHHDIREDVPPKRSRTSTARSYLSGNS 300
OY 301 SLGSMSPSNMEGYSKTOYNQVNPSEDFERAPQSPPTLPK 339
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 SLGSMSPSNMEGYSKTOYNQVNPSEDFERAPQSPPTLPK 339

RESULT 7
OY1W66 PRELIMINARY: PRT: 319 AA.
ID OY1W66
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
OC COSACKIEVIRUS-RECEPTOR HOMOLOG (FRAGMENT).
OS Canis familiaris (Dog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRED GERMAN SHEPHERD; TISSUE=LIVER;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veehel R., Houtsmuller A.B., Schultzeis H.-P.,
RA Lamers J.M.J., Poller W.;
RT "Expression of cosackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers."
RL Gene Ther. 6:1520-1535(1999).
DR EMBL; AF109645; AAF01256.1; -.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_2.
DR SMART; SM00408; IgC2; 1.
DR SMART; SM00410; Ig_Like; 1.
KW Immunoglobulin domain; Receptor.
FT NON_TER 319 319
SQ SEQUENCE 319 AA; 35422 MW; 85C63A6EC7986965 CRC64;

Query Match 81.4%; Score 1545; DB 6; Length 319;
Best Local Similarity 92.2%; Pred. No. 4.8e-129;
Matches 294; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

OY 1 MALLCFVLLCGVADITRSLSTTPPEOMTEKAGETAYLPCTRFLGPEDOGPIIDIEMLLS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MALLCFVLLCGVADITRSLSTTPPEOMTEKAGETAYLPCTRFLGPEDOGPIIDIEMLLS 60
OY 61 PADNOKVQDVIIILYSGDKIYDDYODLKGKRVHTSNDLKSAGASINVTNLQSLDICTYOC 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PADNOKVQDVIIILYSGDKIYDDYODLKGKRVHTSNDLKSAGASINVTNLQSLDICTYOC 120
OY 121 KYKAPGVGNKKIQLTVLKPSTRCYVDGSEIEGDFKLCPEKGSPLYLEMOKLSN 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 KYKAPGVGNKKIQLTVLKPSTRCYVDGSEIEGDFKLCPEKGSPLYLEMOKLSN 180
OY 121 KYKAPGVGNKKIQLTVLKPSTRCYVDGSEIEGDFKLCPEKGSPLYLEMOKLSN 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 KYKAPGVGNKKIQLTVLKPSTRCYVDGSEIEGDFKLCPEKGSPLYLEMOKLSN 180
OY 181 SOKLPTLWLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 SOKTTPSWSTDMTSPVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
OY 241 GAVIGVLLALVILGIVFCCHKKRREKEYEKEVHHDIREDVPPKRSRTSTARSYLSGNS 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 GAVIGVLLALVILGIVFCCHKKRREKEYEKEVHHDIREDVPPKRSRTSTARSYLSGNS 300
OY 301 SLGSMSPSNMEGYSKTOYN 319
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 SLGSMSPSNMEGYSKTOYN 319

RESULT 8
OY1W66 PRELIMINARY: PRT: 372 AA.
ID OY1W66
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
OC COSACKIEVIRUS AND ADENOVIRUS RECEPTOR-LIKE PROTEIN.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20535037; PubMed=11080637;
RA van Raaij M.J., Chouin E., van der Zandt H., Bergelson J.M.,

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RA Cusack S.:
RT "Dimeric structure of the coxsackievirus and adenovirus receptor D1
RL domain at 1.7 Å resolution."
RL Structure 8:1147-1155(2000).
DR EMBL: AF268197; AAK58592.1;
KW Receptor.
SQ SEQUENCE 372 AA; 40664 MW; C363B71E7601C73A CRC64;

Query Match 53.2%; Score 1009; DB 13; Length 372;
Best Local Similarity 50.8%; Pred. No. 2.6e-81;
Matches 189; Conservative 78; Mismatches 89; Indels 16; Gaps 5;

QY 3 LLLCFVLL-----CGVADLTRSLST--TPEOMIERAKGETAYLPCRFITLGPEDGGLDIE 56
DB 8 LCVTVYVLLTSSAGC-----LQITSTGQTSIEKASESVKLDQCFILADSDSPDLIE 60
QY 57 WLLSPADNOKVDYIILYSGKITYDDYQDLKGRVFTSNDLSGDSASINVTNLQSDIG 116
DB 61 WSLQPSDQKEEKYIVYSGRAFEHYDPLKGRVHENSPPKNGDASMNIMGLKATDGT 120
QY 117 TYQCKVKKAPGVGNKKIQLTVLTKPSGTRCVVDSSEELGNFKICEKREGSLPLTYEMO 176
DB 121 TYQCKIKKVPFIASRKYLIVWVRSPKCKSABEGOTYVGMWVLCSSVEBGTQPEYTW 180
QY 177 KLSNSOKLPTLMLAEMTSPVISVKNASTEYSGTYSCTVKNRVGSDOCLRLDVPVPSNR 236
DB 181 RTSNKLPLPLALIDKYTGWTLNATGASGTRCQAKNNGVECEVEYTIQPPMTA 240
QY 237 GTINGAVIGVLLAVLGLVFCCHKRREKREYEHVDIREDPVPPKSTSTARSY-- 294
DB 241 GIINGVYICLLILLLALLLIFCCCRARHKKREKELAYETREDVPPKSRVSTARS 300
QY 295 LGSNHSISGSPSPNMEGYSKTOYNQVSEDEFERAP--QSPITLPLAKVAPNLSRGAVPV 353
DB 301 VGSQRSSISGSPSPNMEYHYSKPYDKITSEYDRPPSHAPLPSPSRMGFWLSRGAIPV 360
QY 354 MIPASOKDSGIV 365
DB 361 MIPANOKDSIV 372

RESULT 9
Q99KGO PRELIMINARY; PRT; 164 AA.
AC 099KGO:
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 17, Last annotation update)
SIMILAR TO COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC004680; AA004680.1; -
DR InterPro: IPR003599; Ig_
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00409; Ig_1.
KW Receptor.
SQ SEQUENCE 164 AA; 17781 MW; 9DEFBDA56240C73 CRC64;

Query Match 33.8%; Score 641; DB 11; Length 164;
Best Local Similarity 86.6%; Pred. No. 4e-49;
Matches 123; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 MALLCFVLLCGVADLTRSLSTTPEOMIERAKGETAYLPCRFITLGPEDGGLDIEWLS 60
DB 11 MALLCFVLLCGVADLTRSLSTTPEOMIERAKGETAYLPCRFITLGPEDGGLDIEWLS 60

DB 1 MALLCFVLLCGIADFTSGLSITTPPEORIERAKGETAYLPCRFITLGPEDGGLDIEWLS 60
QY 61 PADNOKVQVITLYSGDKITYDDYQDLKGRVFTSNDLSGDSASINVTNLQSDIGTYOC 120
DB 61 PSDNOIVDQVITLYSGDKITYDDYQDLKGRVFTSNDLSGDSASINVTNLQSDIGTYOC 120
QY 121 KYKAPGVGNKKIQLTVLTKPS 142
DB 121 KYKAPGVGNKKIQLTVLTKPS 142

RESULT 10
Q9H6B4 PRELIMINARY; PRT; 373 AA.
AC 09H6B4:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CDNA: FLJ22415 FIS, CLONE HRC08561 (HYPOTHETICAL 41.3 KDA PROTEIN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Oktani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE, RHABDOMYOSARCOMA.
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK026068; BAB15347.1; -
DR EMBL: BC009371; AA009371.1; -
DR InterPro: IPR003599; Ig_
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00409; Ig_2.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00410; IGC1like; 1.
KW Immunoglobulin domain; Hypothetical protein.
SQ SEQUENCE 373 AA; 41280 MW; FDA215EB3B3C4335 CRC64;

Query Match 24.8%; Score 471; DB 4; Length 373;
Best Local Similarity 32.6%; Pred. No. 1.7e-33;
Matches 124; Conservative 70; Mismatches 154; Indels 32; Gaps 10;

QY 1 MALLCFVLLCGVADLTRSLSTTPEOMIERAKGETAYLPCRFITLGPEDGGLDIEWLS 60
DB 1 MSLILLILL--VSYYVETLGHTE---IKRAAEKAYVLLPCHQGLGDEKOTLDIEWLLT 54
QY 61 PADNOKVQVITLYSGDKITYDDYQDLKGRVFTSNDLSGDSASINVTNLQSDIGTYOC 120
DB 55 --DNEGNOKVYITVSSRHVNNLTJEOKGRVAFASNFL--AGDASIQIPRLPSDEGRYTC 111
QY 121 KYKAPGVGNKKIQLTVLTKPSGTRCVVDSSEELGNFKICEKREGSLPLTYEMOKL- 178
DB 112 KYKNSGRVWSHVILKIVWVRSPKCKCELEGELTRESDDLTLQESSSGTEPIYIYQRIE 171
QY 179 --SNSOKLPTLMLAEMTSP-VISVKNASTEYSGTYSCTVKNRVGSDOCLRLDVPVPSNR 235
DB 172 KEGBEDERLRPPSRIDYNNRGRVLLONLTMSYSGLQCTAGNDEAGRESGVAVY-IVQYVOS 230
QY 236 AGTAGAVIGVLLAVLGLVFCCHKRREKREYEHV-HDIREDPVPPKSTSTARSY 294
DB 231 IGMVAGAVTGIVAGALLIFLLVWLLIRKDKEREYEEERPNREIDAPARARIVKPS 290

OY 295 IGSNHSLSGSMSPSMEGYSKTOYNQVPEDEFAPOSPFLPLA-----KV 340
 DB 291 SSGSSRSSRSGSSSTRSTANSASRSQRTLSTD--AAPQPLATQAVSLVGEVRSSEPKKV 348
 OY 341 AAPNLSRMCAVPMIPAOSSK 360
 DB 349 HHANLTAKETTPSMIPSOSSR 368

RESULT 11
 O920S5 PRELIMINARY: PRT: 373 AA.

AC O920S5; PRELIMINARY: PRT: 373 AA.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ADIPOCTE-SPECIFIC PROTEIN 5.

OC Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Tsunuga H.;
 RT "Adipocyte-specific protein 5, a novel protein upregulated during
 RT adipocyte differentiation.",
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB040430; BAB6503.1; -
 SO SEQUENCE 373 AA; 41186 MW; 5C62805844F9326 CRC64;

Query Match 23.2%; Score 440.5; DB 11; Length 373;
 Best Local Similarity 31.7%; Pred. No. 8.5e-31;
 Matches 112; Conservative 68; Mismatches 146; Indels 27; Gaps 9;

OY 29 1EKAGETAYLPCRTFLGEDGPDLEWLSPADNOKVDYIILYSGKITDDYDOLK 88
 DB 22 IIRVAEEKVTLPCHHQLGLPERKDTLDIEWLLT--DNEGOKVYITYSRRHYNNLTDEOK 79
 OY 89 GHVHTSNDLKSQDASINTNLQSLDIGTYCKKAPGVNKKIQLTVLTKPSGTRCYV 148
 DB 80 GVAVASNNTL-AGDASLQIEPLKPSDEGRYTKVKNNGYVSHVILKALVPRSKCL 138
 OY 149 DGSIEIGNDFKLCEPKESGLPLLYEMOKL---SNSQRLPPLMLAEMTSP-VISVKNAS 203
 DB 139 EEEPTGESDLTLQCESASGTRPIYVWQRIREKEGDEHLPPKSRIDYNNPRLVLLQNTL 198
 OY 204 TEYSGTGYCTVKNRYSQCLLRLDVPPSNAGTIAAGVIGLALVILGLIVFCCHK 263
 DB 199 MASSGLYOCCTAGNEAGKESCVVR--TVQVOSIGMVAAGVIGVIGALLIFLLIWLIR 257
 OY 264 RREYTERKEVH-HDIREVPPKSRSTFARSYLGSNHSLSGSMSPSMEGYSKTOYNQV 322
 DB 258 KSKDYEEDRNEIREDAEAPRALVPRSSSSSGSSRSRSGSSSTRSGNSASRSQRTL 317
 OY 333 SEDFERAPQSPFL-PLA-----KVAAPNLSRMCAVPMIPAOSSK 360
 DB 318 SS--EAPQQLATQAVSLVGEVRSSEPKKVHHTTLTKAETTLSTTPSOSSK 368

RESULT 12
 O925F2 PRELIMINARY: PRT: 394 AA.
 AC O925F2;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENDOTHELIAL CELL-SELECTIVE ADHESION MOLECULE.
 GN ESAM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SWISS WEBSTER/NIH;
 RX MEDLINE=21238298; PubMed=11279107;
 RA Hirata K.-I., Ishida T., Penta K., Rezaee M., Yang E., Wohlgemuth J.,
 RA Quaternous T.;
 RT "Cloning of an immunoglobulin family adhesion molecule selectively
 RT expressed by endothelial cells."
 RL J. Biol. Chem. 276:16223-16231(2001).
 DR EMBL: AF361882; AAK51504.1; -
 SO SEQUENCE 394 AA; 41810 MW; 302B354943A2227D CRC64;

Query Match 19.0%; Score 360.5; DB 11; Length 394;
 Best Local Similarity 28.9%; Pred. No. 1.2e-23;
 Matches 116; Conservative 73; Mismatches 154; Indels 59; Gaps 15;

OY 3 LLLCEVLLCGVADLTKRS--LSITTPDOMIERAKGETAYLPCRTFLGPD--OGPLDIE- 56
 DB 13 LRVFLGLSTLAAFSRAQELHVPGLNKLAEVGEVVLPAWYTWARESMHPREVP 72
 OY 57 --WLSPADNOKVDYIILYSGDKITDDYDOLKGR--VHFTSNDLKSQDASINTNLQ 112
 DB 73 LITWFL-GEKKEPNQVLSYING-----VMTNKPCTALVH---SISRNVSRLGALOE 121
 OY 113 SDIGTYCKVK-----KAPGVNKKIQLTVLTKPSGTRCYVDSIEINDLKEPKE 166
 DB 122 GSGTGRCSVNVNNDGKRSIGHSIKSIELKVLPRAPRSCSLQGVYVGTNTLNKSPR 181
 OY 167 GSLPLIYEMOKISNSOKL---PFLMLAEMTSPVISVKNASSTEGTCTVKNRSGDQC 223
 DB 182 SKPTAQYQWERLAPSSQVFFGPAL--DAVRGSLKLTNLSIMSGYVCKAONRGVFAKC 238
 OY 224 LRLDVPPSNAGTIAAGVIGLALVLI-GLIVFCCHKRREYTERKEVHHIDREVP 282
 DB 239 NVTLDVMTGS-KAAYVAGVVGTFVGLVILAGLVLL---YORRSKTLDELANDIKEDI 293
 OY 283 PKRSTSTARSYLGSNHSLS-----GSMSPSMEGYSKTOYNQVPS 323
 DB 294 APRTLPTWKGSDTLISKNGTLSSVTSARALRPPKAPPRGTFPTPPSVSSQALLSRRLR 353
 OY 324 EDFERAPQSPFLPLAKVAAPNLSRMCAVPMIPAOSSKDSIV 365
 DB 354 VD-EPPQQLATQAVSLVGEVSSSALSRLMGCAVPMIPAOSSQAGSLV 394

RESULT 13
 O922D5 PRELIMINARY: PRT: 319 AA.
 AC O922D5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GLYCOPROTEIN A33 (TRANSMEMBRANE).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC008528; AAH08528.1; -
 SO SEQUENCE 319 AA; 35692 MW; A37C8DB4BF68C3A CRC64;

Query Match 17.7%; Score 336.5; DB 11; Length 319;
 Best Local Similarity 30.3%; Pred. No. 1.2e-21;
 Matches 88; Conservative 56; Mismatches 113; Indels 33; Gaps 11;

QY 9 LLCVADLRLSLITTPROMIEKAGETAYLPCRFLLGPEQGLDIEW--LLSPADNOK 66
 Db 11 MLCATWAAADLTYETFTODILRAARGSVTLPCYNTNTVSDREG-IQMDKLL-----RSQ 65
 QY 67 VDQYIT--LYSGDKTYDDYODLKGKRVHFTSNDLKSQDASINVTNLQSLDGTGTCCKYK 124
 Db 66 TERVVTNMFVTKKYIYGNRYEN--RVR-VSNDDELNASITIDLTMDMNGTECVSVL 121
 QY 125 ARGV---GNKRIQTLVLLKPGSTRCYVDGSEIGNDFLKEPKEGSLPLYEMOKL--SN 180
 Db 122 MSDQDVNAKSRRLVLPSPKPCDSIOGEMVIGNNIQLTCHSAGSPSPOTSMSKSYNAQ 181
 QY 181 SOKPLTTLMAEMTSPV---ISVKNASTYEGTSCYTKVKNRSGDOCLRLDVPSPNSRA 236
 Db 182 NQGR-----LTQVSESEPLLNKINISTETAGYICTSSNDVIGIESCINITAAPRPSNNI 235
 QY 237 GTTGAVALGVALVGLIGLIVFCCKKRREKEVHHDRDPKPS 286
 Db 236 ALYAGIAGVFAVALLIIGVIVYCCCKRREKDDKDD-----REDARPNRA 279

RESULT 14

Q95K13 PRELIMINARY; PRT: 390 AA.
 ID Q95K13
 AC Q95K13
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYOTHETICAL 40.9 KDA PROTEIN.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_Taxid=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TEMPORAL LOBE RIGHT;
 RA Osaka N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 libraries."
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 RW EMBL; AB060855; BAB46874.1;
 KW Hypothetical protein.
 SQ SEQUENCE 390 AA; 40946 MW; CDBF63F2BD464EF5 CRC64;

Query Match 17.7%; Score 335.5; DB 6; Length 390;
 Best Local Similarity 27.2%; Pred. No. 1.9e-21;
 Matches 111; Conservative 69; Mismatches 153; Indels 75; Gaps 15;

QY 3 LLCVLLCGVADLRLS--LSITTPROMIEKAGETAYLPCRFLLGPE---DQGLD-IE 56
 Db 13 LRLFLGLSALAPPSRAELOHLRANOLAVEGGEVLPAMVTLAEVSSAOPGEVPPVM 72
 QY 57 WLLSPADNOKVDOYIILYSG-----DKIYDDYODLKGKRVHFTSNDLKSQDASINVT 108
 Db 73 WEFK--DKEKEDQVLSYINGVTTSKPGVSLV-----SMPSRNLSIRLE 114
 QY 109 NLQSLDGTGTCCKYK-----KAPGVGNKKIQLVLLKPGSTRCYVDGSEIIGNDFKLK 162
 Db 115 GLQEKDSQPSGCVNVDKNGASGHSIKTLELNVLPAPPSRCLQGVPRVGAHVTLSC 174
 QY 163 EPKESGSLPLYEMOKLSOKLPLMLAEMTSPV-----ISVKNASTYEGTSCYTKY 215
 Db 175 QSPNSKPAVOITQMDR-----QLPFS--FOTFRAPVLDVIRGSLSLNLSMAGVYCAAH 227
 QY 216 NRVGSDOCLRLDVPSPNSRAGTIGAVIGVALLVGLIGLIVFCCKKRREKEVHHDRDPKPS 275
 Db 228 NEVGTAQCNVTL--VSTGPGAIVAVGAVGTIVGLLGLVLLH---RRKALDEPRAN 283
 QY 276 DIREP-----VPPKSTRTSTARSTLGSNHSL-----GSMSPSMMBEGYSKTO 317

Db 284 DIKEDAIAPRLTPMPKSSDTISKNGTSSVTSARALRPPHGPBPRLGALTPPSSLSSOALP 343
 QY 318 YNQVSESEDERAPQSEPTLPLAKVAAPNLSRMKAVPMIPMAQSKDSIV 365
 Db 344 SPRLPTTDGAN-PQPISTLIPGVSSTGLSRMGAVPMVPAQSOASGLV 390

RESULT 15

Q9CV44 PRELIMINARY; PRT: 304 AA.
 ID Q9CV44
 AC Q9CV44
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE 2210413P10RIK PROTEIN (FRAGMENT).
 CN 2210413P10RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=STOMACH;
 RX MEDLINE=21085660; PubMed=11217851;
 RX Kawai J., Shimagawa A., Shibata K., Konno H., Aachi Y., Fukuda S.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Aachi Y., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuwiel P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Obofelli D., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Garibolai M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombearts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyszynski B.A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK008920; BAB25968.1;
 DR MGD; MGI:1919617; 2210413P10RIK.
 DR InterPro; IPR003599; I9.
 DR InterPro; IPR003598; I9_C2.
 DR InterPro; IPR003006; I9_MHC.
 DR InterPro; IPR003596; I9_V.
 DR Pfam; PF00047; I9_2.
 DR SMART; SM00409; I9; 2.
 DR SMART; SM00408; IGC2; 2.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin domain.
 FT NON_TER 304
 SQ SEQUENCE 304 AA; 31919 MW; 522BA38898AD7A9F CRC64;

Query Match 17.3%; Score 327.5; DB 11; Length 304;
 Best Local Similarity 31.3%; Pred. No. 7e-21;
 Matches 91; Conservative 45; Mismatches 132; Indels 23; Gaps 10;

QY 4 LLCVLLCGVADLRLS--LSITTPROMIEKAGETAYLPCRFLLGPEQGLDIEW--LLSPA 62
 Db 14 LGLFVCLSLA-----VEVTLPTEPLSPKGTALSLSCYSYGVGN--FALEMSFVQPG 66
 QY 63 DQKQDVQVYIILYSGDKTYDDYODLKGKRVHFTSNDLKSQDASINVTNLQSLDGTGTCCKY 122
 Db 67 KRISASVPLVLTNGHLVPT--GSKADRAIILHDPPTGLATILKLTDLRPSDTGTYLCAV 124
 QY 123 KRAP-----GVGNKKIQLVLLKPGSTRCYVDGSEIIGNDFKLKPEKESGSLPLYEMOK 177

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 2002, 13:46:33 ; Search time 28.31 Seconds
(without alignments)
499.210 Million cell updates/sec

Title: US-09-899-634A-4
Perfect score: 1898
Sequence: 1 MALLICFVLGCVADLTRSL.....SRMGAVPMIPAKSKGSIIV 365

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1754	92.4	365	1 CXAR_HUMAN	P78310 homo sapien
2	1739	91.6	365	1 CXAR_MOUSE	P97792 mus musculu
3	368.5	19.4	319	1 A33_HUMAN	O99795 homo sapien
4	197	10.4	299	1 JAM1_HUMAN	O99624 homo sapien
5	186	9.8	298	1 JAM2_HUMAN	P57087 homo sapien
6	170	9.0	298	1 JAM1_BOVIN	O99756 bos taurus
7	161.5	8.5	306	1 CD80_MOUSE	O00609 mus musculu
8	160.5	8.5	300	1 JAM1_MOUSE	O88792 mus musculu
9	152.5	8.0	538	1 PVR2_HUMAN	O92692 homo sapien
10	151	7.9	526	1 CEAL_HUMAN	P13688 homo sapien
11	149	7.9	740	1 PECT1_PIG	O95242 sus scrofa
12	148.5	7.8	727	1 PECT1_MOUSE	O08481 mus musculu
13	148.5	7.8	764	1 ICCR_DROME	O08180 drosophila
14	148	7.8	526	1 BUTY_BOVIN	P18882 bos taurus
15	146.5	7.7	519	1 ECTO_RAT	P16573 rattus norv
16	145.5	7.7	517	1 PVR1_HUMAN	O15223 homo sapien
17	139.5	7.3	738	1 PECT1_HUMAN	P16284 homo sapien
18	137.5	7.2	515	1 PVR1_PIG	O99176 sus scrofa
19	136.5	7.2	3707	1 PGBM_MOUSE	O05793 mus musculu
20	136	7.2	309	1 CD80_MOUSE	P42082 mus musculu
21	134	7.1	355	1 C166_CARAU	O90304 carassius a
22	133	7.0	329	1 CD80_HUMAN	O13410 homo sapien
23	133	7.0	526	1 BUTY_HUMAN	P42081 homo sapien
24	133	7.0	530	1 PVR2_MOUSE	P32507 mus musculu
25	132	7.0	515	1 PVR1_MOUSE	O99766 mus musculu
26	131.5	6.9	348	1 KIL0_RAT	O92018 rattus norv
27	130.5	6.9	1070	1 PTK7_HUMAN	O13360 homo sapien
28	130	6.8	837	1 NCN2_MOUSE	O35136 mus musculu
29	128.5	6.8	4393	1 PGBM_HUMAN	P98160 homo sapien
30	127.5	6.7	344	1 NTR1_RAT	O62718 rattus norv
31	127	6.7	246	1 MYP0_HENFR	P20998 heterodontu
32	126.5	6.6	564	1 C166_BRARE	O90460 brachydanio
33	125.5	6.6	739	1 VCA1_HUMAN	P19320 homo sapien

34	124.5	6.6	847	1 CD22_HUMAN	P20273 homo sapien
35	124.5	6.6	858	1 NCAL_RAT	P13596 rattus norv
36	124	6.5	521	1 CEAL_MOUSE	P53789 mus musculu
37	124	6.5	1336	1 VGR1_RAT	P53789 rattus norv
38	123.5	6.5	417	1 PVR_CERAE	P32506 ceratopithe
39	123	6.5	1906	1 KML5_CHICK	P11799 gallus gall
40	122.5	6.5	811	1 FS22_DROME	P34083 drosophila
41	122.5	6.5	873	1 FS21_DROME	P34082 drosophila
42	122	6.4	215	1 C1B2_RAT	P54900 rattus norv
43	122	6.4	837	1 NCN2_HUMAN	O15394 homo sapien
44	122	6.4	1036	1 AXO1_CHICK	P28685 gallus gall
45	121	6.4	219	1 MYP0_BOVIN	P10522 bos taurus

ALIGNMENTS

RESULT 1
CXAR_HUMAN STANDARD; PRT; 365 AA.
ID P78310: 000694:
AC 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cocksackievirus and adenovirus receptor precursor (Cocksackievirus B-
DE adenovirus receptor) (hCAR) (CVB3 binding protein).
GN CXADR OR CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=971910109; PubMed=9036860;
RX Tomko R.P., Xu R., Philipson L.,
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Cocksackie B viruses and
RT adenoviruses 2 and 5.";
RT Science 275:1320-1323(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97250541; PubMed=9096397;
RA Tomko R.P., Xu R., Philipson L.,
RA "hCAR and hCAR: the human and mouse cellular receptors for subgroup C
RT adenoviruses and group B coxsackieviruses.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20008750; PubMed=10543405;
RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
RA Bowles N.E.;
RT "Genomic organization and chromosomal localization of the human
RT Cocksackievirus B-adenovirus receptor gene.";
RT Hum. Genet. 105:354-359(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Anderson C.W., Kieletzawa J., Dunn J.J., Freimuth P.;
RT "Sequence and expression of CXADR, the human gene for the
RT coxsackievirus and adenovirus receptor.";
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
CC - FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
CC SUBCELLULAR LOCATION: TYPE I membrane protein.
CC - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC - SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC	EMBL	Y07593	CAA68868.1	;-	
DR	EMBL	U90716	AAC51234.1	;-	
DR	EMBL	AF169366	AAAF05908.1	;-	
DR	EMBL	AF169360	AAAF05908.1	JOINED.	
DR	EMBL	AF169361	AAAF05908.1	JOINED.	
DR	EMBL	AF169362	AAAF05908.1	JOINED.	
DR	EMBL	AF169363	AAAF05908.1	JOINED.	
DR	EMBL	AF169364	AAAF05908.1	JOINED.	
DR	EMBL	AF169365	AAAF05908.1	JOINED.	
DR	EMBL	AF200465	AAAF2434.1	;-	
DR	MM	602621		;-	
DR	InterPro	IPR003006	IG_MHC.		
DR	InterPro	IPR003598	IG_C2.		
DR	InterPro	IPR003600	IG_1like.		
DR	Flam	PF00047	Ig; 2.		
DR	SMART	SM00410	IG_1like; 1.		
DR	SMART	SM00408	IGC2; 1.		
KM	Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal.				
Repeat.					
	SIGNAL	1	19	POTENTIAL.	
FT	CHAIN	20	365	COSACKAITEYRUS AND ADENOVIRUS RECEPTOR.	
FT	DOMAIN	20	237	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	238	258	POTENTIAL.	
FT	DOMAIN	259	365	CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN	34	127	IG-LIKE C2-TYPE DOMAIN 1.	
FT	DOMAIN	155	219	IG-LIKE C2-TYPE DOMAIN 2.	
FT	DISULFID	41	120	BY SIMILARITY.	
FT	DISULFID	162	212	BY SIMILARITY.	
FT	CARBOHYD	106	106	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	201	201	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SO	SEQUENCE	365 AA;	40029 MW;	AB01C6346CB/EB54 CRC64;	

Query Match	92.4%;	Score 1754;	DB 1;	Length 365;
Best Local Similarity	90.7%;	Pred. No. 3.1e-126;		
Matches 331; Conservative	16;	Mismatches 18;	Indels 0;	Gaps 0

QY	1	MALLICFVILCGVADLTRSLSTITTPEQMIKAKGETAYLPCRFILGIPEDQGPLDIEMWLS	60
Db	1	MALLICFVILCGVADFEARSLSTITTPREMIKAKGETAYLPCKFLTSPEDQPLDIEMWLS	60
QY	61	PADNOKVQVYIIILYSGDKITDYDYQDLKGRHFNLSNDLSGDSASINTNQLSDIGTYQC	120
Db	61	PADNOKVQVYIIILYSGDKITDYDYPRDLKGRHFNLSNDLSGDSASINTNQLSDIGTYQC	120
QY	121	KYKKAAPGVGNKKIOLTVYLKPSGTRCYVDGSEEIFGNDFKLCBEPCEGSLPLIYEMOKLSN	180
Db	121	KYKKAAPGVGNKKIHLVYLKPSGARCYVDGSEEIFGSPFKICEPKBESLPLQIYEMOKLSD	180
QY	181	SOKLEPTLWLAEMTSPVIVKNAASIEYSGTYSCTYKKNRYSQDLRLDYVPSPSNRAGTIA	240
Db	181	SOKMPTSMIAEMTSSVIVKNAASIEYSGTYSCTYKRNRRGSPQCLRLRYVPSPSKAKGLIA	240
QY	241	GAVIEVLLATLVILGILIVCECHKKRREKEEYKEKEVHHDIREDVPPPKSRTSTARSLGSNHS	300
Db	241	GAIITFLALALILGILITCCKKRREKEEYKEVHHDIREDVPPPKSRTSTARSLGSNHS	300
QY	301	SIGSMSPSNMEGYSKTOYNQVPSSEDEFERAPOSPILLAKYAAPNLISRMGAVPVIIPAQSK	360
Db	301	SIGSMSPSNMEGYSKTOYNQVPSSEDEFERTPOSPILLPAKVAAPNLISRMGAIIPVMIIPAQSK	360
QY	361	DGSIY 365	
Db	361	DGSIY 365	
RESULT	2		
CXAR_MOUSE		STANDARD:	PRT: 365 AA.
ID	CXAR_MOUSE		
AC	P979792: 009052:		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		

01-MAR-2002 (Rel. 41, Last annotation update)
Coxsackievirus and adenovirus receptor homolog precursor (mCAR).
CN CxADR OR CAR. (Mouse).
OS Mus musculus. (Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_taxid=10090;
[1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Liver;
RC MEDLINE=97190109; PubMed=9036660;
RX Bergeon J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horvitz M.S., Crowell R.L., Flinberg R.W.;
RT "Isolation of a common receptor for Coxsackieviruses and
RL adenoviruses 2 and 5.";
RN Science 275:1320-1323(1997).
[2]
SEQUENCE FROM N.A.
RP STRAIN=C3H/MAI;
RC MEDLINE=97250541; PubMed=9096397;
RX Tomko R.P., Xu R., Philipson L.;
RA "The murine CAR homologue (mCAR) is a receptor for coxsackie B
RT viruses and adenoviruses.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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DR EMBL: Y10320; CAA71368.1; -.
DR EMBL: U90715; AAC53148.1; -.
DR EMBL: Y11929; CAAT7679.1; -.
DR MGD: MGI:1201679; Cxadr.
DR InterPro: IPRO003006; IG_MHC.
DR InterPro: IPRO003598; IG_C2.
DR InterPro: IPRO03600; IG_Like.
DR Pfam: PF00047; Ig_2.
DR SMART: SMO0410; IG_Like; 1.
DR SMART: SMO0408; IGC2; 1.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
Repeat.
KW SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 365 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR
FT CHAIN HOMOLOG.
FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 238 258 POTENTIAL.
FT DOMAIN 259 365 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 155 219 IG-LIKE C2-TYPE DOMAIN 2.
FT DISULFD 41 120 BY SIMILARITY.
FT DISULFD 162 212 BY SIMILARITY.
FT CARBOHD 106 106 N-LINKED (GLCNAc...) (POTENTIAL).
FT CARBOHD 201 201 N-LINKED (GLCNAc...) (POTENTIAL).
FT CONFLICT 340 365 VAAINTSMGVAIPWPIAPOSQDSGISIV -> EKVIYKIDGIT
VV (IN REF. 2 AND 3).
SQ SEQUENCE 365 AA: 39947 MW: 5445B4B52A34B2A2 CKG64;

Query Match 91.6%; Score 1739; DB 1; Length 365;

Best Local Similarity 90.4%; Pred. No. 4.2e-125;
Matches 330; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

```

QY 1 MALLLCVLLCGVADLTRSLSTTPPEOMIEKAGETAYLPCRTFLGPDGDPDIDIELLS 60
DB 1 MARLLCFLVLLCGIADLFTSGITTPPEQRIKAKETAYLPCCKFLSPEDGDPDIDIELLS 60
QY 61 PADNOKVDQYIILYSGDKIYDDYQDLKGRVHFTSNDLKSADASINTNLQSLDIGTYQC 120
DB 61 PSDNQIYDQYIILYSGDKITDNTYPLDKGRVHFTSNDVKSADASINTNLQSLDIGTYQC 120
QY 121 KVKKAPGVNKKIOLTVLLKPSGTCRYDGSSEIIGNDFKLKCEKESLPLLYEMOKLSN 180
DB 121 KVKKAPGVNKKIOLTVLLKPSGTCRYDGSSEIIGNDFKLKCEKESLPLLYEMOKLSN 180
QY 181 SQRKPTMLAEMTSPTVSVNANSTEGTSCYTKNRVSGDCLLRDVPVPSRAGTIA 240
DB 181 SQRKPTMLAEMTSPTVSVNANSTEGTSCYTKNRVSGDCLLRDVPVPSRAGTIA 240
QY 241 GAVIGVLLALVLLGLIVFCCHKKRREKYEVEVHHDIREDVPPKSTARSYLSGNSH 300
DB 241 GAVIGVLLALVLLGLIVFCCHKKRREKYEVEVHHDIREDVPPKSTARSYLSGNSH 300
QY 301 SLGSMSPSNMEGYSKYQYNOVPESEFERAPQSPPLAKYAAPNLSPMGAVPVMIPQSK 360
DB 301 SLGSMSPSNMEGYSKYQYNOVPESEFERAPQSPPLAKYAAPNLSPMGAVPVMIPQSK 360
QY 361 DGSTV 365
DB 361 DGSTV 365

```

RESULT 3

```

A33_HUMAN STANDARD: PRT: 319 AA.
ID A33_HUMAN
AC Q99795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cell surface A33 antigen precursor (Glycoprotein A33).
GN GPA33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Colon carcinoma;
MDLINE=97165045; PubMed=9012807;
Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
Mortiz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
Scott A.M., Rittler G., Cohen L., Welt S., Old L.J., Nice E.C.,
Burgess A.W.;
RA "The human A33 antigen is a transmembrane glycoprotein and a novel
RT member of the immunoglobulin superfamily."
RT Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
RN [2]
RP POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=97396159; PubMed=9245713;
RA Rittler G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
Mortiz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
Simpson R.J.;
RT "Characterization of posttranslational modifications of human A33
RT antigen, a novel palmitoylated surface glycoprotein of human
RT gastrointestinal epithelium."
RL Biochem. Biophys. Res. Commun. 236:682-686(1997).
CC -1- FUNCTION: MAY PLAY A ROLE IN CELL-CELL RECOGNITION AND SIGNALING.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NORMAL GASTROINTESTINAL
CC EPITHELIUM AND IN 95% OF COLON CANCERS.
CC -1- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 K OF N-LINKED
CC CARBOHYDRATE.
CC -1- PTM: PALMITOYLATED.

```

```

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-----
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-----
CC EMBL: U79725; AAC50957.1; -
CC HSSP: P06907; INEU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00410; Ig_Like; 1.
DR SMART: SM00406; Ig; 1.
KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW Transmembrane; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 319
FT DOMAIN 22 235
FT TRANSMEM 236 256
FT DOMAIN 257 319
FT DOMAIN 36 124
FT DOMAIN 139 229
FT DOMAIN 258 261
FT DISULFID 43 117
FT DISULFID 162 211
FT DISULFID 146 222
FT CARBOHYD 112 112
FT CARBOHYD 200 200
FT CARBOHYD 223 223
SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AFAF45C2408E CRC64;
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Query Match 19.4%; Score 368.5; DB 1; Length 319;
Best Local Similarity 30.9%; Pred. No. 5.9e-21;
Matches 99; Conservative 62; Mismatches 128; Indels 31; Gaps 13;
-----
QY 10 LCGVADLTRSLSTTPPEOMIEKAGETAYLPCRTFLGPDGDPDIDIELLS 66
DB 12 LCAVRVTVDALISVETPDVILRASOGKSVTLPCYHTSTSSREGI-10MDKLLLT-----H 65
QY 67 VDOYIILYSGDK--IYDDYQDLKGRVHFTSNDLKSADASINTNLQSLDIGTYQCKVKR 124
DB 66 TERVIVIPFENKNYTHIELT---KNRYSI--SNNAEQSDASITIDQLTMAONGTYECVS 121
QY 125 APGV-GNKK--IOLTVLLKSGTRCYDGSSEIIGNDFKLKCEKESLPLLYEMOKLS-N 180
DB 122 MSDEGNTKSRVRLVLPVPSKPECGIEGETIIGNNTQLTQCSKEGSPFOYSKRRYNIL 181
QY 181 SQRKPTMLAEMTS-PTVSVNANSTEGTSCYTKNRVSGDCLLRDVPVPSRAGT 239
DB 182 NQEP---LAQPSAGQPVSLKSNISTDTSGYITCSSNEEGTFCNTIVAVRSPSNVALY 238
QY 240 AGAVIGVLLALVLLGLIVFC---HKKRREKYEVEVHHDIREDVPPKSTARS 292
DB 239 VGIAVGVAALLIIGIILYCCCGKNDNEDKRDAPNNAEVEPEQJRLSREHEE 298
QY 293 -SYGSHSSLSGSKSPSME 311
DB 299 DDYKQEQRSTGREGSPDHL 318
-----
RESULT 4
JAM1_HUMAN STANDARD: PRT: 299 AA.
ID JAM1_HUMAN
AC Q9Y624;

```

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion
 DE molecule 1) (PAM-1) (Platelet FII receptor).
 GN JAMI OR JCAM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99323940;
 RA Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
 RA Iwamatsu A., Kita T.;
 RT "Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes
 RT redistribution of junctional adhesion molecule in human endothelial
 RT cells.";
 RL J. Immunol. 163:553-557(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Sobočka M.B., Sodocki T., Rushbrook J.I., Banerjee P., Weiss C.,
 RA Konecki E.;
 RT "Molecular cloning and sequencing of the cDNA of FII receptor, a
 RT novel Ig superfamily member from human platelets.";
 RL submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX Naik U.P., Naik M.U., Deleon P., Spychala J.;
 RT "Cloning and characterization of PAM-1, a novel platelet adhesion
 RT molecule involved in platelet activation.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Brain;
 RL MEDLINE=21154917; Pubmed=11230166;
 RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
 RA Ansorge W., Boeher M., Bloecher H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
 RA Wewes H.-W., Ottenwelder B., Obermaler B., Tampe J., Heubner D.,
 RA Wandut R., Korn B., Klein M., Pouscka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 RT analysis of 500 novel complete protein coding human cDNAs.";
 RL Genome Res. 11:422-435(2001).
 CC CC
 CC -I- FUNCTION: PLAYS A ROLE IN REGULATING MONOCYTE TRANSmigration
 CC INVOLVED IN INTEGRITY OF EPITHELIAL BARRIER. INVOLVED IN PLATELET
 CC ACTINATION.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -I- TISSUE SPECIFICITY: LOCALIZED AT TIGHT JUNCTIONS OF BOTH
 CC EPITHELIAL AND ENDOTHELIAL CELLS.
 CC -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -I- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
 CC -----
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 CC -----
 CC DR EMBL, AF111713; AAD42050.1; -
 DR EMBL, AF207907; AAF2829.1; -
 DR EMBL, AF172398; AAD48877.1; -
 DR EMBL, AL136649; CAB6584.1; -
 DR MIM: 605721; -
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SMO0410; Ig_Like; 1.
 DR SMART: SMO0406; IGV_1.
 KM Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;

Query Match	Best Local Similarity	10.4%	Score 197;	DB 1;	Length 299;
Matches 73;	Conservative 43;	Mismatches 108;	Indels 54;	Gaps 14;	
QY 1	MALLCFLVLCGVADLTSLSTTPPEQMIKAKGTATLPCEFT--LGPEDGPDIEML 58	FT SIGNAL 1	25	POTENTIAL.	
DB 12	LCLFLALLILCSLA--LGSVTVHSEPEVRIPENNPNVLLSCAYSCSFSSPR-----VEKK 63	FT CHAIN 1	26	JUNCTIONAL ADHESION MOLECULE 1.	
QY 59	LSPADNOKVDVVIILYSGDKIYDDYODLKGRHPTSDNLKSGDASINVTNLQSDIGTY 118	FT DOMAIN 1	26	EXTRACELLULAR (POTENTIAL).	
DB 64	FDGGDTTR----LVCYN-NKITASY-----EDRVFE----LPTGIFKSVTR---EDFGTY 107	FT TRANSMEM 1	239	POTENTIAL.	
QY 119	QCKYKAKAG--VGKKIOLTVLLKPSGTRCYVDGSEELGNDFKLCEPKREGSLPLLTQ 176	FT DOMAIN 1	238	CYTOPLASMIC (POTENTIAL).	
DB 108	TCMVSEEGNSGYGEKVKVLIIVLPSPKPTVPIPSATIGNRAVLVLCSDSDSPSEYTW 167	FT DOMAIN 1	239	IG-LIKE V-TYPE DOMAIN 1.	
QY 177	K-----LSNKSQKPTLMLEEMTSPVSYVKNASREXSGTSCYKKNVGSQ 222	FT DOMAIN 1	239	IG-LIKE V-TYPE DOMAIN 2.	
DB 168	KDGIYMPNPKSTRAFSSTVLPNTTIGELVDPDLISASD-----TGEYSCEARNGYGT 222	FT DISULFID 1	146	POTENTIAL.	
QY 223	C--LLRLDVPVPSNRAGTIAGAVIGVLLALVIGLIVE 258	FT DISULFID 1	153	POTENTIAL.	
DB 223	TSNAVMEAV--ERNVGIVTAA--VLVTLLILGLIVE 255	FT CARBOHYD 1	185	N-LINKED (GLCNAC. . .) (POTENTIAL).	
RESULT 5		SO SEQUENCE	299 AA;	32583 MM;	D95DE2FEA23D2851 CRC64;
JAM2_HUMAN	STANDARD;	PRT;	298 AA.		
AC P57087;					
DT 16-OCT-2001 (Rel. 40, Created)					
DT 16-OCT-2001 (Rel. 40, Last sequence update)					
DT 01-MAR-2002 (Rel. 41, Last annotation update)					
DE junctional adhesion molecule 2 precursor (Vascular endothelial					
DE junction-associated molecule) (VE-JAM).					
DE JAM2 OR C21ORF43.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX NCBI_Taxid:9606;					
LN 11					
RP SEQUENCE FROM N.A.					
RC TISSUE=Vascular endothelial cells;					
RX MEDLINE=20317114; PubMed=10779521;					
RA Palmeri D., Van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;					
RT "Vascular endothelial junction-associated molecule, a novel member of					
RT the immunoglobulin superfamily, is localized to intercellular					
RT boundaries of endothelial cells ";					
RL J. Biol. Chem. 275:19139-19145(2000).					
RN 12					
RN SEQUENCE FROM N.A.					
RP TISSUE=Placenta;					
RX MEDLINE=20507930; PubMed=10945976;					
RA Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjerkke R.J.,					
RA Vanderslice P., Morris A.P., Brock T.A.;					
RT "A novel protein with homology to the junctional adhesion molecule:					
RT characterization of leukocyte interactions ";					
RT J. Biol. Chem. 275:34750-34756(2000).					
CC -!- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO					
CC SECONDARY LYMPHOID ORGANS.					

```

CC -1- SUBCELLULAR LOCATION: type I membrane protein (potential).
CC -1- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL
CC VENUES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.
CC LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
CC CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF25910; AAF8123.1; -.
CC EMBL: AY016009; AAG49022.1; -.
CC InterPro: IPR003006; Iq.MHC.
CC InterPro: IPR003598; Iq.C2.
CC InterPro: IPR003600; Iq.Like.
CC Pfam: PF00047; Iq; 2.
CC SMART: SM00410; Iq_Like; 1.
CC SMART: SM00410; Iq_Like; 1.
CC Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
CC
CC FT SIGNAL 1 20 POTENTIAL.
CC FT CHAIN 21 298 JUNCTIONAL ADHESION MOLECULE 2.
CC FT DOMAIN 21 238 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 239 259 POTENTIAL.
CC FT DOMAIN 260 298 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 43 116 IG-LIKE V-TYPE DOMAIN.
CC FT DOMAIN 148 221 IG-LIKE C2-TYPE DOMAIN.
CC FT DISULFID 50 109 POTENTIAL.
CC FT DISULFID 155 214 POTENTIAL.
CC FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC
CC SO SEQUENCE 298 AA; 33207 MW; CA7BE518E22DCAEE CRC64;

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Query Match 9.8%; Score 186; DB 1; Length 298;
 Best Local Similarity 24.5%; Pred. No. 4.1e-07;
 Matches 82; Conservative 49; Mismatches 136; Indels 68; Gaps 12;

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QY 1 MALLLCVLLCGVADLTFRSLSTTPPEOMIEKAGETAYLCRFLGPDGPDIDIEMLLS 60
   :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 10 LLLLRLLVALLGKAYGFSAPRQDQVAVVEYQEAFLACK--TPKKTVSSRLV--- 63
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   PADNOKVDQVYIIYSGDKIYDDYQ-----DLGRVHFTSNDLKSQDASINVTQLSDI 115
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 64 -----KRL-----GSSVGFVYVYQQLQGDFFKRAEMI-----DFNIRIKNVTSDA 104
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 116 GTYQCKVKKAPGVGNKKIQ-----LTVLLKPSGTRCYVDSEETGDNFKLCEPKESLP 170
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 105 GKRYCEV-SAPSEGGOMLEEDTVLELVAPVPSCEVPSSALSGTVLELRCQDKEGPA 163
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 171 LLYEMOK-----LSN-----SQKLPTLWLAEMTSVIVSKNASTFYSCTYCKNRRGSD 221
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 164 PEYTWFDGIRLENPRLGSGSTNSSTYTMNTKGTQLQFNVTYSKLDTEYSCEARNVGYR 223
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 222 QCLRLVLPVPPSNRAGTIAAGVIGVLLALVLIIGLIVFCCHKRREREKREVEHHDIEDV 281
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 224 RCPCKRQVODLNISGLIA-AVVYVALVIVSGIGV--CYAQR----- 263
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 282 PPKSRTSTARSTYSGNHSLSGSPSNMEGYST 316
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 264 ---KGYSKETSFOKSNSSSKATMTMSNDPFRHTKS 295
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 6
 JAM1_BOVIN STANDARD; PRT; 298 AA.

```

AC 09XT56;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Junctional adhesion molecule 1 precursor (JAM).
GN JAM1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99323940; PubMed=10395639;
RA Ozaki H., Iishi K., Horiiuchi H., Arai H., Kawamoto T., Okawa K.,
RA Iwamatsu A., Kita T.;
RT Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes
RT redistribution of junctional adhesion molecule in human endothelial
RT cells."
RL J. Immunol. 163:553-557(1999).
CC -1- FUNCTION: PLAYS A ROLE IN REGULATING MONOCYTE TRANSLOCATION
CC INVOLVED IN INTEGRITY OF EPITHELIAL BARRIER. INVOLVED IN PLATELET
CC ACTIVATION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: type I membrane protein (potential).
CC -1- TISSUE SPECIFICITY: LOCALIZED AT TIGHT JUNCTIONS OF BOTH
CC EPITHELIAL AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF111714; ABD42051.1; -.
CC InterPro: IPR003006; Iq.MHC.
CC InterPro: IPR003598; Iq.C2.
CC InterPro: IPR003600; Iq.Like.
CC Pfam: PF00047; Iq; 2.
CC SMART: SM00410; Iq_Like; 1.
CC SMART: SM00408; IqC2; 1.
CC
CC KW Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
CC Repeat; Signal.
CC
CC FT SIGNAL 1 24 POTENTIAL.
CC FT CHAIN 25 298 JUNCTIONAL ADHESION MOLECULE 1.
CC FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 238 258 POTENTIAL.
CC FT DOMAIN 259 298 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 42 115 IG-LIKE V-TYPE DOMAIN 1.
CC FT DOMAIN 145 218 IG-LIKE V-TYPE DOMAIN 2.
CC FT DISULFID 49 108 POTENTIAL.
CC FT DISULFID 152 211 POTENTIAL.
CC FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC
CC SO SEQUENCE 298 AA; 32456 MW; 714FE1C1714769A2 CRC64;

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Query Match 9.0%; Score 170; DB 1; Length 298;
 Best Local Similarity 25.5%; Pred. No. 6.7e-06;
 Matches 70; Conservative 41; Mismatches 113; Indels 50; Gaps 13;

```

QY 3 LLLCFVLLCGVADLTFRSLSTTPPEOMIEKAGETAYLCRFT--LGEPDGPDIDIEMLLS 60
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 13 LLLFTSMILCSIA-LGR-AVQTYEPVVPENNPALKSCSYSGSSPR-----VEWKF 64
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 61 PADNOKVDQVYIIYSGDKIYDDYQDLKGRVHFTSNDLKSQDASINVTQLSDIGTYQC 120
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 65 HGDIRG---LVCTN-NKITASY-----ENRYTSS-----DIGITHSTYTRKDTGMYTC 108
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 121 KVKKAPG--VGNNKIQLTVLLKPSGTRCYVDGSEETGDNFKLCEPKESGLPLLYEMOK- 177
   :||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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DB 109 MWSDEGNTGYEVTVQVLIVLPSPKPTINVPSSVTIGTAVLTGSEKSDSPSEKWEKD 168
 QY 178 -----LSNSOKLPTLMLAEMTSPVYSKNASTEXSGTYKVRKNSDQCL 224
 DB 169 GVEMLPEKSNRAPSNS-----SYTLNOKTGELI-FDPVSAPTGPTGCAQNGVSP--- 220
 QY 225 LRLDVPPSNRAGTITAGAVIGLALVLGLIV 258
 DB 221 VKSDTVHMDAVELNVGIVAAVFTLLILGALIF 254

RESULT 7
 CD80_MOUSE STANDARD: PRT: 306 AA.
 AC 000609;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen) (B7).
 CD80 OR B7.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE-B-cell;
 RC MEDLINE=91341422; PubMed=1714935;
 RA Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J., White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
 "Structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7.";
 J. Exp. Med. 174:625-631(1991).
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE-B-cell;
 RC MEDLINE=93307789; PubMed=768531;
 RA Selvakumar A., White P.C., Dupont B.;
 "Genomic organization of the mouse B-lymphocyte activation antigen B7.";
 Immunogenetics 38:292-295(1993).
 CC -1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL MALIGNANCIES.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND ITS EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
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 CC
 DR EMBL: X60958; CAA43291.1;
 DR EMBL: L12589; AAA37240.1; ALT. SEQ.
 DR EMBL: L12585; AAA37240.1; JOINED.
 DR EMBL: L12586; AAA37240.1; JOINED.
 DR EMBL: L12587; AAA37240.1; JOINED.
 DR EMBL: L12588; AAA37240.1; JOINED.
 DR PIR: S17291; S17291.
 DR MGI:101775; Cd80.

DR InterPro: IPR003599; IG_MHC.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003600; IG_1like.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00409; Ig; 1.
 DR SMART: SM00410; IG_1like; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane; Receptor.
 FT SIGNAL 1 37
 FT CHAIN 38 306
 FT DOMAIN 38 246
 FT TRANSMEM 247 268
 FT DOMAIN 269 306
 FT DOMAIN 47 126
 FT DOMAIN 158 226
 FT DOMAIN 227 246
 FT DISULFID 54 119
 FT DISULFID 165 219
 FT CARBOHYD 93 93
 FT CARBOHYD 99 99
 FT CARBOHYD 149 149
 FT CARBOHYD 189 189
 FT CARBOHYD 210 210
 FT CARBOHYD 214 214
 SQ SEQUENCE 306 AA; 34589 MW; 1DBADE0931B84C62 CRC64;

Query Match 8.5%; Score 161.5; DB 1; Length 306;
 Best Local Similarity 23.2%; Pred. No. 3.1e-05;
 Matches 68; Conservative 56; Mismatches 110; Indels 59; Gaps 14;

QY 3 LLLCVLLCGVADLRLRSSTTPPEMIRKAGETVILPCRFLEGGDGPDIEMLLSPA 62
 DB 1 LILFVLLIRLSQVSSD-----DQLSKSVKDKVLLPCRRNSPHEDESDRTW----- 70
 QY 63 DNQKVDVYII-LYSGD-KIYDYYODLKGVRHFTSNDSKSDASINYNLQSDIGTYQC 120
 DB 71 --QKIDKVLVSIAKGLKLVPEY-----KNRTLYDNTY-----SLIILGLVLSDGITSC 119
 QY 121 KYKAPGVGNKKIQLTVLLKPS-----GTRCYVDGSEIGNDFKLCPEKGSILPLYEW 175
 DB 120 VVQKKER-GTYEVKHLALVVKLSIKADFSTPNITESGNSADPKRTYCPASGGFPKPRESW 178
 QY 176 OKLSQKPLPTLMLAEMTSPVYSKNAST--EYSSTYCTYKVRKNSDQCLRL----- 227
 DB 179 --LENGRELPGINTTISDPESELTYTSSQDLFNTTRHTK-----CLIKYGDAHVS 229
 QY 228 -----DVPSPSNRAGTITAGAVIGLALVLGLIV--FCCHK--RREE 267
 DB 230 EDFWEKEPDEPPDSKNLVLFGAGFAGVITVIVLILKCFKRRSCFRNE 282

RESULT 8
 JAM1_MOUSE STANDARD: PRT: 300 AA.
 AC 088792;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Junctional adhesion molecule 1 precursor (JAM).
 GN JAM1 OR JCAM1 OR JCAM.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98327120; PubMed=9660867;
 RA Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M., Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A., Simmons D., Dejana E.;
 "Junctional adhesion molecule, a novel member of the immunoglobulin superfamily that distributes at intercellular junctions and modulates

```

RT      monocytic transmigration." ;
RL      J. Cell Biol. 142:117-127(1998) .
CC      -I- FUNCTION: PLAYS A ROLE IN REGULATING MONOCYTE TRANSMIGRATION
CC      INVOLVED IN INTEGRITY OF EPITHELIAL BARRIER. INVOLVED IN PLATELET
CC      ACTIVATION.
CC      -I- SUBCELLULAR LOCATION: Type I membrane protein (Potential) .
CC      -I- TISSUE SPECIFICITY: LOCALIZED AT TIGHT JUNCTIONS OF BOTH
CC      EPITHELIAL AND ENDOTHELIAL CELLS.
CC      -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC      -I- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch) .
CC      -----
DR      EMBL, U89915: AAC32982.1; .
DR      MGP, MGI:1321398; Jcam1.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003600; Ig_Like.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig_2.
DR      SMART; SM00410; Ig_Like; 1.
DR      SMART; SM00406; Igv; 1.
DR      K1, K2, K3, K4, K5, K6, K7, K8, K9, K10, K11, K12, K13, K14, K15, K16, K17, K18, K19, K20, K21, K22, K23, K24, K25, K26, K27, K28, K29, K30, K31, K32, K33, K34, K35, K36, K37, K38, K39, K40, K41, K42, K43, K44, K45, K46, K47, K48, K49, K50, K51, K52, K53, K54, K55, K56, K57, K58, K59, K60, K61, K62, K63, K64, K65, K66, K67, K68, K69, K70, K71, K72, K73, K74, K75, K76, K77, K78, K79, K80, K81, K82, K83, K84, K85, K86, K87, K88, K89, K90, K91, K92, K93, K94, K95, K96, K97, K98, K99, K100, K101, K102, K103, K104, K105, K106, K107, K108, K109, K110, K111, K112, K113, K114, K115, K116, K117, K118, K119, K120, K121, K122, K123, K124, K125, K126, K127, K128, K129, K130, K131, K132, K133, K134, K135, K136, K137, K138, K139, K140, K141, K142, K143, K144, K145, K146, K147, K148, K149, K150, K151, K152, K153, K154, K155, K156, K157, K158, K159, K160, K161, K162, K163, K164, K165, K166, K167, K168, K169, K170, K171, K172, K173, K174, K175, K176, K177, K178, K179, K180, K181, K182, K183, K184, K185, K186, K187, K188, K189, K190, K191, K192, K193, K194, K195, K196, K197, K198, K199, K200, K201, K202, K203, K204, K205, K206, K207, K208, K209, K210, K211, K212, K213, K214, K215, K216, K217, K218, K219, K220, K221, K222, K223, K224, K225, K226, K227, K228, K229, K230, K231, K232, K233, K234, K235, K236, K237, K238, K239, K240, K241, K242, K243, K244, K245, K246, K247, K248, K249, K250, K251, K252, K253, K254, K255, K256, K257, K258, K259, K260, K261, K262, K263, K264, K265, K266, K267, K268, K269, K270, K271, K272, K273, K274, K275, K276, K277, K278, K279, K280, K281, K282, K283, K284, K285, K286, K287, K288, K289, K290, K291, K292, K293, K294, K295, K296, K297, K298, K299, K300, K301, K302, K303, K304, K305, K306, K307, K308, K309, K310, K311, K312, K313, K314, K315, K316, K317, K318, K319, K320, K321, K322, K323, K324, K325, K326, K327, K328, K329, K330, K331, K332, K333, K334, K335, K336, K337, K338, K339, K340, K341, K342, K343, K344, K345, K346, K347, K348, K349, K350, K351, K352, K353, K354, K355, K356, K357, K358, K359, K360, K361, K362, K363, K364, K365, K366, K367, K368, K369, K370, K371, K372, K373, K374, K375, K376, K377, K378, K379, K380, K381, K382, K383, K384, K385, K386, K387, K388, K389, K390, K391, K392, K393, K394, K395, K396, K397, K398, K399, K400, K401, K402, K403, K404, K405, K406, K407, K408, K409, K410, K411, K412, K413, K414, K415, K416, K417, K418, K419, K420, K421, K422, K423, K424, K425, K426, K427, K428, K429, K430, K431, K432, K433, K434, K435, K436, K437, K438, K439, K440, K441, K442, K443, K444, K445, K446, K447, K448, K449, K450, K451, K452, K453, K454, K455, K456, K457, K458, K459, K460, K461, K462, K463, K464, K465, K466, K467, K468, K469, K470, K471, K472, K473, K474, K475, K476, K477, K478, K479, K480, K481, K482, K483, K484, K485, K486, K487, K488, K489, K490, K491, K492, K493, K494, K495, K496, K497, K498, K499, K500, K501, K502, K503, K504, K505, K506, K507, K508, K509, K510, K511, K512, K513, K514, K515, K516, K517, K518, K519, K520, K521, K522, K523, K524, K525, K526, K527, K528, K529, K530, K531, K532, K533, K534, K535, K536, K537, K538, K539, K540, K541, K542, K543, K544, K545, K546, K547, K548, K549, K550, K551, K552, K553, K554, K555, K556, K557, K558, K559, K560, K561, K562, K563, K564, K565, K566, K567, K568, K569, K570, K571, K572, K573, K574, K575, K576, K577, K578, K579, K580, K581, K582, K583, K584, K585, K586, K587, K588, K589, K590, K591, K592, K593, K594, K595, K596, K597, K598, K599, K600, K601, K602, K603, K604, K605, K606, K607, K608, K609, K610, K611, K612, K613, K614, K615, K616, K617, K618, K619, K620, K621, K622, K623, K624, K625, K626, K627, K628, K629, K630, K631, K632, K633, K634, K635, K636, K637, K638, K639, K640, K641, K642, K643, K644, K645, K646, K647, K648, K649, K650, K651, K652, K653, K654, K655, K656, K657, K658, K659, K660, K661, K662, K663, K664, K665, K666, K667, K668, K669, K670, K671, K672, K673, K674, K675, K676, K677, K678, K679, K680, K681, K682, K683, K684, K685, K686, K687, K688, K689, K690, K691, K692, K693, K694, K695, K696, K697, K698, K699, K700, K701, K702, K703, K704, K705, K706, K707, K708, K709, K710, K711, K712, K713, K714, K715, K716, K717, K718, K719, K720, K721, K722, K723, K724, K725, K726, K727, K728, K729, K730, K731, K732, K733, K734, K735, K736
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DR DT 16-OCT-2001 (Rel. 40, Last sequence update)
DR DT 16-MAR-2002 (Rel. 41, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Herpes virus entry
GN mediator B) (HvB) (Nectin 2) (CD112 antigen).
GN PVRL2 OR PRR2 OR HVBL.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95347610; PubMed=7622062;
RA Eberle F., Dubreuil P., Mattel M.-G., Devillard E., Lopez M.;
RT "The human PRR2 gene, related to the human poliovirus receptor gene
RL (PVR), is the true homolog of the murine MPH gene.";
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=98321161; PubMed=9657005;
RA Wainer M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
RA Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
RT "A cell surface protein with herpesvirus entry activity (HvEB) confers
RT susceptibility to infection by mutants of herpes simplex virus type
RT 1, herpes simplex virus type 2, and pseudorabies virus.";
RL Virology 246:179-189(1998).
RN [3]
RP SEQUENCE OF 31-538 FROM N.A.
RA Yoshiura K., Murray J.C.;
RT "A transcriptional map in the region of 19q13 derived using direct
RT sequencing and exon trapping.";
RN Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 449-538 FROM N.A.
RX MEDLINE=99449047; PubMed=10520737;
RA Freitas L.K., Zhang W.J., Lalonde J.P., Tay G.K., Gaudieri S.,
RA Ashworth L.K., Van Bockxmeer F.M., Dawkins R.L.;
RT "Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene:
RT PERCL.";
RL DNA Seq. 9:89-101(1998).
CC -I- FUNCTION: RECEPTOR FOR ALPHAHHERPESVIRUS (HSV-1, HSV-2 AND
CC PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS, ALPHA AND DELTA (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -I- TISSUE SPECIFICITY: UBIQUITOUS.
CC -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -I- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -I- DATABASE: NAME=PROV, NOTE=CD guide CD112 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/204270028_g.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X80038; CAA56342.1; -
DR EMBL: AF058448; AAC23797.1; -
DR EMBL: AF044968; AAC82348.1; -
DR EMBL: AF044962; AAC82348.1; JOINED.
DR EMBL: AF044963; AAC82348.1; JOINED.
DR EMBL: AF044964; AAC82348.1; JOINED.
DR EMBL: AF044966; AAC82348.1; JOINED.
DR EMBL: AF044967; AAC82348.1; JOINED.
DR EMBL: AF050154; AAD02503.1; -
DR MIM: 600798; -
DR InterPro: IPR003599; IG.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG; 3.
DR SMART: SM00409; IG; 1.

```


FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 357 357 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 436 436 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 740 AA: 82378 MW: F312DC62C4BA4217 CRC64;

Query Match 7.9%; Score 149; DB 1; Length 740;
Best Local Similarity 23.5%; Pred. No. 0.00087;
Matches 58; Conservative 44; Mismatches 115; Indels 30; Gaps 8;

QY 84 YODLGRVHFTSNDLKSQDASINVTNLSIDIGTQOC---KYKAPGVGNKKIQLTVLLK 140
DB 443 YOLLKSGDSLASONVSNBPFAVKDN-PTKDV-EYOCIDNCHSHAGMPSKYLRAVVIAP 500
QY 141 PGTGRCYVDGSEI--GNDFKLCPEKESPLYLEMOKLSNOKPLTLMLEMTSPVIS 198
QY 501 VEEVKISILSEEVESGAIYLCQSVKESGSPITTKFYKEKEKRPHTVLTND-TOALWH 559
QY 199 VKNASTESGTYSCYVKNRFGSDCLRLDVP---PSNRAGTAGAVIGVLLALVLI 253
DB 560 KKKASMDQGOYCYCLASNRATPSKNEFLQSNILAVRYVLAIPWKKGLAVVAVIIVLL 619
QY 254 GLIVFCCHKKRREKYEKEVHNDRVPPKSRSTARSYLGSNHSLSGMSPSMEGY 313
DB 620 GARFFFLKSKAKOM-----PYEMCRPAAPLINSNEK--TLSDPNTKAN 662
QY 314 SKTOYNO 320
DB 663 RHYGYNE 669

RESULT 12
PECL MOUSE
ID - PECL MOUSE STANDARD: PRT: 727 AA.
AC 008481:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Platelet endothelial cell adhesion molecule precursor (PECAM-1)
DE (CD31 antigen).
GN PECAM1 OR PECAM-1 OR PECAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
QY NCBI_Taxid=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-Lung;
RX MEDLINE=93296179; PubMed=8516303;
RA Xie Y., Muller W.A.;
RT "Molecular cloning and adhesive properties of murine
platelet/endothelial cell adhesion molecule 1";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5569-5573(1993).
[2]
SEQUENCE OF 18-26.
RP TISSUE=Heart;
RC MEDLINE=93035639; PubMed=1415479;
RA Bogen S.A., Baldwin H.S., Watkins S.C., Albelda S.M., Abbas A.K.;
RT "Association of murine CD31 with transigrating lymphocytes following
antigenic stimulation";
RL Am. J. Pathol. 141:843-854(1992).
CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE EXPRESSED ON
PLATELETS AND AT ENDOTHELIAL CELL INTERCELLULAR JUNCTIONS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL: I06039; AAA16230.1; -.
DR MGI: MGI:97537; Pecam.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00409; IG; 1.
DR SMART: SM00410; IG_Like; 2.
KW Immunoglobulin domain; Glycoprotein; Cell adhesion; Transmembrane;
KW Repeat; Phosphorylation; Signal.
FT SIGNAL 1 17
FT CHAIN 18 727
FT DOMAIN 18 590
FT TRANSMEM 591 609
FT DOMAIN 610 727
FT DOMAIN 40 106
FT DOMAIN 135 203
FT DOMAIN 238 300
FT DOMAIN 329 382
FT DOMAIN 413 472
FT DOMAIN 505 568
FT DISULFID 47 99
FT DISULFID 142 195
FT DISULFID 245 293
FT DISULFID 336 375
FT DISULFID 420 465
FT DISULFID 512 561
FT CARBOHYD 74 74
FT CARBOHYD 141 141
FT CARBOHYD 309 309
FT CARBOHYD 345 345
FT CARBOHYD 360 360
FT CARBOHYD 424 424
FT CARBOHYD 540 540
FT MOD_RES 702 702
FT CONFLICT 18 18
SQ SEQUENCE 727 AA: 81262 MW: 34C04752D199BAA5 CRC64;

Query Match 7.8%; Score 148.5; DB 1; Length 727;
Best Local Similarity 21.8%; Pred. No. 0.00093;
Matches 61; Conservative 51; Mismatches 127; Indels 41; Gaps 10;

QY 84 YODLGRVHFTSNDLKSQDASINVTNLSIDIGTQOCYKKA---PYGNKKIQLTVLLK 140
DB 431 YHLMKAKSDFOLEVTYSNDPA-TFTDKPTRDM-EYOCRADNCHSHPAVFSELRLRVLIAP 488
QY 141 PGTGRCYVDGSEI--GNDFKLCPEKESPLYLEMOKLSNOKPLTLMLEMTSPVIS 198
DB 489 VDEVVITSLSNVEVSGSMVLRCSYKVECTSPITTFQFYKEKEDRRFHQA-VYNDQAFNH 547
QY 199 VKNASTESGTYSCYVKNRFGV-----SDQCLRLDVPSPNRAGTAGAVIGVLLALV 251
DB 548 NKQASKKQGOYCYCLASNRATPSKNEFLQSNILAVRYVLAIPWKKGLAVVAVIIVLL 605
QY 252 LGLIVFCCHKKRREKYEKEVHNDRVPPKSRSTARSYLGSNHSLSGMSPSMNE 311
DB 606 IYAANCYFLRKAKAKOK-----PVEMSRPAAPLINSNSEKI--SEPSVE 647
QY 312 GYSKTOYNOVSEDF-----BRAPSPYLLPLAKVAAPRL 345
DB 648 ANSHGYDDVSGNDAAVKNPKQNDPQNDVETVEVSSL 687

RESULT 13
ICCR_DROME
ID ICCR_DROME STANDARD: PRT: 764 AA.

AC Q00180; 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Irregular chiasm C-roughnest protein precursor (IRREC protein).
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94102535; PubMed=7503814;
 RA Ramos R.G., Igloi G.L., Lichte B., Baumann U., Meier D.,
 RA Schneider T., Brandstaetter J.H., Froehlich A., Fischbach K.-F.;
 RT "The irregular chiasm C-roughnest locus of Drosophila, which affects
 axonal projections and programmed cell death, encodes a novel
 immunoglobulin-like protein.";
 RL Genes Dev. 7:2533-2547(1993).
 CC -1- FUNCTION: REQUIRED FOR CORRECT AXONAL PATHWAY FORMATION IN
 THE OPTIC LOBE AND FOR PROGRAMMED CELL DEATH IN THE DEVELOPING
 RETINA.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: POSTEMBRYONIC EXPRESSION IS STRONG IN THE
 DEVELOPING OPTIC LOBE AND IN THE EYE IMAGINAL DISC.
 CC -1- DEVELOPMENTAL STAGE: STRONGLY EXPRESSED IN EMBRYOS. ALSO FOUND
 IN LATE LARVAL AND PUPAL STAGES.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 DR EMBL: Z21641; CAA79756.1; -;
 DR EMBL: L11040; AAA16632.1; -;
 DR PIR: A49448; A49448.
 DR PIR: S34129; S34129.
 DR HSSP: P56276; ITLK.
 DR FLYBase: F8gn0003285; rsl.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00410; IG_Like; 4.
 DR SMART: SM00408; IGC2; 1.
 KM Transmembrane; Immunoglobulin domain; Glycoprotein; Signal; Repeat;
 KW Cell adhesion.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 764 IRREGULAR CHIASM C-ROUGHNEST PROTEIN.
 FT DOMAIN 20 533 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 534 556 POTENTIAL.
 FT DOMAIN 557 764 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 115 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 137 221 IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 245 261 GLY-RICH.
 FT DOMAIN 325 332 IG-LIKE C2-TYPE DOMAIN 3.
 FT DOMAIN 353 414 IG-LIKE C2-TYPE DOMAIN 4.
 FT DOMAIN 432 515 IG-LIKE C2-TYPE DOMAIN 5.
 FT DOMAIN 637 660 GLN-RICH (OPA-REPEAT).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 764 AA; 82947 MW; 262225DB2BA1C181 CRC64;

Query Match 7.8%; Score 148.5; DB 1; Length 764;
 Best Local Similarity 18.0%; Pred. No. 0.00099;
 Matches 71; Conservative 62; Mismatches 122; Indels 139; Gaps 14;
 QY 15 DLTRSLSTTPQMIKAKGETAVLPCEFTUGPEDQGLDLEWLSPADNCKVDQVILY 74
 DB 341 DISVAPSRQRPQSWAEADVGSVSLTCEVDSNPQPELWIOHPSD----- 385
 QY 75 SGDIRYDDYDLDKGRVHFTSNDLKSQDASINVMQLSDIGTQCK----- 121
 DB 386 -----RVVGSTNL-----TFSVSN-----ETAGRIYCKANPQVLEISADA 422
 QY 122 ---VKAPGVGNKRIQTLVTLKPSGTRCYVDG-----SEEGNDFKLC 162
 DB 423 YVILKGSALISQRTQYGLVDFTARECFASSVPARHVSMTFNGQELSSSGHDYSLY 482
 QY 163 EPEKGSPLLEYKWKLSNSOKPLTLMLEMTSPVSVKNASTEISGTYKRVNGSDO 222
 DB 483 DAVPGV-----KSTLLIRDSQAHYHGKYNCTVVDYNDGV 518
 QY 223 CLLRDVPVPSNRAGTING-AVIGVILALVLGLIVFCCHKRR-----EEKYK- 271
 DB 519 AEIQLOAKKSVSLMTITVGGISVAVFLVLTILVVYIKCKRKRLPPADYISEHQTKN 578
 QY 272 -----EVHNDIREDV-----PPKSRSTARSYLSGNSHSLG 303
 DB 579 GGVSCKLEPGRTSNYSDLKADISGGYVPYGDYSTHSPPPQYLTCTK---SNGSS-- 633
 QY 304 SMSPSNMEGYSKTYNOVPSDFERAPQSPPLPL 337
 DB 634 TIMONNHQNLQLOOQOOSH-HQHHTQTTLPLM 666
 RESULT 14
 ID BUTY_BOVIN STANDARD; PRT; 526 AA.
 AC P18892; O18955; O18959;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Butyrophillin precursor (Bt).
 GN BTN1A1 OR BTN.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
 RX MEDLINE=90354441; PubMed=3387867;
 RA Jack L.J.W., Mather I.H.;
 RT "Cloning and analysis of cDNA encoding bovine butyrophillin, an apical
 glycoprotein expressed in mammary tissue and secreted in association
 with the milk-fat globule membrane during lactation.";
 RT J. Biol. Chem. 265:14481-14486(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HOLSTEIN-FRIESIAN;
 RA Davey H.W., Ogg S.L., Husaini Y., Snell R.G., Korobko I.V.,
 RA Mather I.H., Wilkins R.J.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Seyfert H., Luethen F.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=95293916; PubMed=7775382;
 RA Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.;
 RT "Site-specific glycosylation of bovine butyrophillin.";
 RL J. Biochem. 117:147-157(1995).
 CC -1- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT

CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
 CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
 CC ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@sdb.ch).

CC EMBL; M35551; AAB39766.1; -
 CC EMBL; AF005497; AAB62889.1; -
 CC EMBL; Z93323; CAB07533.1; -
 CC PIR: A37821; A37821.
 CC InterPro: IPR001870; Gamma_carboxylase.
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR003596; Ig_V.
 CC InterPro: IPR003877; SPRY.
 CC InterPro: IPR003878; SPRY_domain.
 CC Pfam: PF00047; Ig; 1.
 CC Pfam: PF00622; SPRY; 1.
 CC SMART: SM00406; IGV; 1.
 CC SMART: SM00449; SPRY; 1.
 CC Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 CC SIGNAL 1 26
 CC CHAIN 27 526 BUTYROPHILIN.
 CC DOMAIN 27 242 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 243 269 POTENTIAL.
 CC DOMAIN 270 526 CYTOPLASMIC (POTENTIAL).
 CC CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
 CC CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (HYBRID).
 CC CONFLICT 35 35 O -> P (IN REF. 3).
 CC CONFLICT 230 230 E -> D (IN REF. 1).
 CC SEQUENCE 526 AA; 59276 MW; A14126802BD19284 CRC64;

Query Match 7.8%; Score 148; DB 1; Length 526;
 Best Local Similarity 22.5%; Pred. No. 0.00066;
 Matches 67; Conservative 53; Mismatches 126; Indels 52; Gaps 11;

QY 4 LIGFVLLCGVADRLRSLSITTPPEOMIEKAGETAVLPCHFTLGPEDQPLDIETW---LS 60
 DB 13 LLIFFLLDLPKIDSPAFVDVIGQPEPLAVAGDAELPCRLSPNVSAAKQ-MEDIRWEFKS 71
 QY 61 PADNKGVOVILLISGDKRYDDYODDKGRVHFTSNDLSKSGASINVTNLOLSIDICTYOC 120
 DB 72 PA-----VEFSREGQEGEGEEMAEYRGVSLVEDHIAEGSAVARIQEKSDDEYRC 124
 QY 121 KYKKAQGVGNKKIQLTVLLKPSGTRCYVDGSEEGNDEKFKC-----EPR-----EG 167
 DB 125 PFRQDENEEALVHLKV--AALGSDPHISMKYQEGSEIOLLECTSGVWYEPDQVOMTHNG 182
 QY 168 SLPLLYENOKLSNOKLPLTLLAEMTSPIV---SVKNASTEGSGTYCTVKNRSGSDOC 223
 DB 183 E-----EPPMSSESRNPDEEGELTVRASVYIIRDSMKNV-----SCCINLLIGQEK 229
 QY 224 LRLDVP-----PSNRAGTAGAVIGVLLAVLIGLIVPCCH-----KKRREKYEKE 272
 DB 230 EYESVSPASFPRLLPMPVAVAVILVIGLLTIGSLFTWRLYKERSRORRNEFFSSKE 287

RESULT 15
 PCTO_RAT

ID ECTO_RAT STANDARD: PRT; 519 AA.
 AC P16573;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ecto-ATPase precursor (Cell-CAM 105) (C-CAM 105) (ATP-dependent
 DE taurocholate-carrier protein) (Gp110).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-68.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
 RX MEDLINE=89340561; PubMed=2527235;
 RA Lin S.-H., Guidotti G.;
 RT "Cloning and expression of a cDNA coding for a rat liver plasma
 RT membrane ecto-ATPase. The primary structure of the ecto-ATPase is
 RT similar to that of the human biliary glycoprotein I.";
 RL J. Biol. Chem. 264:14408-14414(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY, AND WISTAR; TISSUE=Liver;
 RX MEDLINE=93279310; PubMed=8504806;
 RA Edlund M., Gaardsvoll E., Bock E., Oedbrink B.;
 RT "Different isoforms and stock-specific variants of the cell adhesion
 RT molecule C-CAM (cell-CAM 105) in rat liver.";
 RL Eur. J. Biochem. 213:1109-1116(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
 RX MEDLINE=92344597; PubMed=1637321;
 RA Culic O., Huang Q., Flanagan D., Hixson D., Lin S.-H.;
 RT "Molecular cloning and expression of a new rat liver cell-CAM105
 RT isoform. Differential phosphorylation of isoforms.";
 RL Biochem. J. 285:47-53(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=94058980; PubMed=8240240;
 RA Cheung P.H., Culic O., Qiu Y., Earley K., Thompson N., Hixson D.C.,
 RA Lin S.-H.;
 RT "The cytoplasmic domain of C-CAM is required for C-CAM-mediated
 RT adhesion function: studies of a C-CAM transcript containing an
 RT unspliced intron.";
 RL Biochem. J. 295:427-435(1993).
 RN [5]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=90292222; PubMed=2141577;
 RA Auriavillius M., Hansen O.C., Lazrek M.B.S., Bock E., Oedbrink B.;
 RT "The cell adhesion molecule Cell-CAM 105 is an ecto-ATPase and a
 RT member of the immunoglobulin superfamily.";
 RL FEBS Lett. 264:267-269(1990).
 RN [6]
 RP PARTIAL SEQUENCE.
 RC STRAIN=WISTAR; TISSUE=Liver;
 RX MEDLINE=93292517; PubMed=8513803;
 RA Becker A., Lucka L., Kilian C., Kannicht C., Reutter W.;
 RT "Characterisation of the ATP-dependent taurocholate-carrier protein
 RT (Gp110) of the hepatocyte canalicular membrane.";
 RL Eur. J. Biochem. 214:539-548(1993).
 RN [7]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=93123234; PubMed=8380406;
 RA Najjar S.M., Accilli D., Philippe N., Jernberg J., Margolis R.,
 RA Taylor S.I.;
 RT "ppl20/ecto-ATPase, an endogenous substrate of the insulin receptor
 RT tyrosine kinase, is expressed as two variably spliced isoforms.";
 RL J. Biol. Chem. 268:1201-1206(1993).
 RN [8]
 RP CHARACTERIZATION.
 RX MEDLINE=91354197; PubMed=1831973;
 RA Lin S.-H., Culic O., Flanagan D., Hixson D.C.;

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GenCore version 4.5
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OW protein - protein search, using sw model

Run on: May 11, 2002, 12:48:43 ; Search time 42.66 Seconds
(without alignments)
822.143 Million cell updates/sec

Title: US-09-899-634A-4
Perfect score: 1898
Sequence: 1 MALLICFVLICGVADLFRSL.....SRMGAVPMVIPAQSKGSIV 365

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	197	10.4	299	2	S56749
2	164.5	8.7	483	2	T17346
3	160.5	8.5	1091	2	A58532
4	159.5	8.4	4162	2	T42633
5	159	8.4	5175	2	T20992
6	159	8.4	5198	2	T43290
7	157.5	8.3	309	2	I49503
8	152.5	8.0	538	2	I68093
9	151	8.0	526	1	A32164
10	151	8.0	7962	2	I38346
11	150	7.9	518	2	JC4024
12	148.5	7.8	764	2	A49448
13	148	7.8	526	2	A37821
14	146.5	7.7	519	2	A44783
15	145.5	7.7	509	2	JC5288
16	144.5	7.6	513	2	JC5289
17	139.5	7.3	738	2	A40096
18	137.5	7.2	398	2	I49443
19	136.5	7.2	3707	2	S18252
20	136	7.2	309	2	I49522
21	134	7.1	523	2	I50478
22	133	7.0	329	1	A48754
23	133	7.0	526	2	S70587
24	133	7.0	530	2	A53437
25	132	7.0	1070	2	JC4593
26	131	6.9	1323	2	PN0568
27	129.5	6.8	478	2	I33960
28	129.5	6.8	4391	2	A38096
29	127.5	6.7	344	2	I56551

30	127.5	6.7	503	2	JC5287	SHP substrate-1 pr
31	127	6.7	246	1	A32999	myelin P0 protein
32	126.5	6.7	464	2	C30127	transmembrane carc
33	126	6.6	521	2	S34338	billary glycoprote
34	126	6.6	824	2	S36439	fibroblast growth
35	125.5	6.6	739	2	B41288	vascular cell adhe
36	125.5	6.6	792	2	A41288	vascular cell adhe
37	125.5	6.6	847	2	JH0371	B-cell adhesion pr
38	124.5	6.6	647	2	A35648	B-cell adhesion pr
39	124.5	6.6	858	1	IURTNC	neural cell adhesi
40	124	6.5	521	2	JC1508	billary glycoprote
41	124	6.5	1336	2	I60598	Fit-1 tyrosine kin
42	123.5	6.5	417	2	A44194	poliovirus recepto
43	123.5	6.5	538	2	JC2457	vascular cell adhe
44	123.5	6.5	2222	2	T13924	sdh protein - frui
45	123	6.5	1227	2	T23004	hypothetical prote

ALIGNMENTS

RESULT 1
S56749
Junctional adhesion molecule precursor - human
N:Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F
C:Species: Homo sapiens (man)
C>Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: A59406; S56749
R:Osaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.
J. Immunol. 163, 553-557, 1999
A:Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistrib
A:Reference number: A59406; PMID:99333940; PMID:10395639
A:Accession: A59406
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <OZA>
A:Cross-references: GB:AAD42050; NID:95326797; PIDN:AAD42050.1
R:Maik, U.P.; Ehrlich, Y.R.; Kornecki, E.
Biochem. J. 310, 155-162, 1995
A:Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking o
A:Reference number: S56749; PMID:95374438; PMID:7646439
A:Accession: S56749
A:Molecule type: protein
A:Residues: 28-49, 'X', 51-53; 62-73, 'E', 75-103; 123, 'F', 125-130; 'PDKDITLYLNXX'; 'LF', 206,
A:Note: the order of the peptides other than the amino terminus was not determined
C:Genetics:
A:Gene: JAK
C:Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-299/Product: junctional adhesion molecule #status predicted <MAT>

Query Match 10.4% Score 197; DB 2; Length 299;
Best Local Similarity 26.3%; Pred. No. 7.8e-07;
Matches 73; Conservative 43; Mismatches 108; Indels 54; Gaps 14;
QY 1 MALLICFVLICGVADLFRSLITPEQMIKAKETAYLCORF--LGPEDQGLDLEWL 58
Db 12 LCFILAILICSLA--LGSVTHSSSEPEVRIPENPKLSCAVSGFSSPR-----VEWK 63
QY 59 LSPADNOKVDVILLYSGDKYIDYDYLKGRVHFTSNDLKSQDASINVTNLQSLDIGTY 118
Db 64 FDSQDTR-----LVCYN-NKITASY-----EDRVTF-----LPTGITFSVTR---EDGTY 107
QY 119 QCVKKAAPG--VGNKKITQLTVLLKPSGTRCYVDGSEIGDKFKCEPKESGLPLLEYWQ 176
Db 108 TCWVSEEGGNSYGEVKKLIVLPSPKPTVNPISATIGNRAVLTCSEODGSPSEYTW 167
QY 177 K-----LSNSOKPLTMLAEMTSPIYSVKNASTEVSGYGVCTVKNRVSDD 222
Db 168 KDGIVMPNPKSTRFAFNSSVLVNPTTGGELVFDPLDLSAD-----TGLEYSCAARGYGT 222
QY 223 C--LLRIDVVPSPNRAGTIGAVIGVLLAVLGLIIVF 258

Db 223 TSNAMREAV--ERNVGVIVAA---VLVTLLGLITVF 255

RESULT 2

T17346 hypothetical protein DKFZp58601624.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T17346

R:Dusterheft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

Submitted to the Protein Sequence Database, September 1999

A:Reference number: Z18727

A:Accession: T17346

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-483 <DUE>

A:Cross-references: EMBL:AL117666

A:Experimental source: adult uterus; clone DKFZp58601624

Genetics:

Gene: DKFZp58601624.1

Query Match 8.7%: Score 164.5; DB 2; Length 483;
Best Local Similarity 25.3%; Pred. No. 0.00031;
Matches 62; Conservative 41; Mismatches 117; Indels 25; Gaps 7;

107 VTNILOSDIGYQCKVKAPGVGNKKIQLTTLKPSGRCYVDGSEELGNDKCEPKE 166

Db 49 ITDVKIDDAAGVYSCTAQNSAGSISANATITVLETSPVLPLEDRVAVGCEYALOCK AT 107

107 VTNILOSDIGYQCKVKAPGVGNKKIQLTTLKPSGRCYVDGSEELGNDKCEPKE 166

Db 108 GNPPIRITWFKGDRPLSTERHHLTPDQQLVYQNVVAEDAGRVCENSLGTERRASQ 167

108 GNPPIRITWFKGDRPLSTERHHLTPDQQLVYQNVVAEDAGRVCENSLGTERRASQ 167

108 GNPPIRITWFKGDRPLSTERHHLTPDQQLVYQNVVAEDAGRVCENSLGTERRASQ 167

108 GNPPIRITWFKGDRPLSTERHHLTPDQQLVYQNVVAEDAGRVCENSLGTERRASQ 167

108 GNPPIRITWFKGDRPLSTERHHLTPDQQLVYQNVVAEDAGRVCENSLGTERRASQ 167

108 GNPPIRITWFKGDRPLSTERHHLTPDQQLVYQNVVAEDAGRVCENSLGTERRASQ 167

108 GNPPIRITWFKGDRPLSTERHHLTPDQQLVYQNVVAEDAGRVCENSLGTERRASQ 167

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108 GNPPIRITWFKGDRPLSTERHHLTPDQQLVYQNVVAEDAGRVCENSLGTERRASQ 167

F:262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F:286-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:310-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F:334-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F:358-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F:382-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F:409-432/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F:440-485/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 8.5%: Score 160.5; DB 2; Length 1091;
Best Local Similarity 24.6%; Pred. No. 0.00177;
Matches 68; Conservative 43; Mismatches 124; Indels 41; Gaps 11;

34 GETAYLPCRFITLGPEDQPLDIEMWLSPADQKVDVYILYSGDKTYDDYQDLKGRVHF 93

Db 615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

34 GETAYLPCRFITLGPEDQPLDIEMWLSPADQKVDVYILYSGDKTYDDYQDLKGRVHF 93

Db 615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

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615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

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615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

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615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

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615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

615 GTTARLECAATGHPNPQ---IAW-----QK-----DGG---TDPRARERRRHV 652

RESULT 3

trial cell membrane glycoprotein LIG-1 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999

C:Accession: A58532

R:Suwaki, Y.; Sato, N.; Tohyama, M.; Manaka, A.; Takag, T.

J. Biol. Chem. 271, 22522-22527, 1996

A:Title: cDNA cloning of a novel membrane glycoprotein that is expressed specifically in

A:Reference number: A58532; MUID:96394313

A:Accession: A58532

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1091 <SUZ>

A:Cross-references: GB:D78572; NID:g1545806; PIDN:BA11416.1; PID:g1545807

C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan amino-ter

F:36-61/Domain: proteoglycan amino-terminal homology <PAH>

F:71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>

F:95-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>

F:118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>

F:142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>

F:166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>

F:191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>

F:214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>

F:238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>

RESULT 4

connectin/titin - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C:Accession: T42633

R:Tajima, H.; Ohtsuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.;

Biochem. Biophys. Res. Commun. 223, 160-164, 1996

A:Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin

A:Reference number: 222221; MUID:96234045

A:Accession: T42633

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-4162 <YAJ>

A:Cross-references: EMBL:D83390; NID:g1513029; PIDN:BA11908.1; PID:g1513030

A:Experimental source: breast muscle

C:Keywords: skeletal muscle

Query Match 8.4%: Score 159.5; DB 2; Length 4162;
Best Local Similarity 25.6%; Pred. No. 0.011;
Matches 61; Conservative 38; Mismatches 90; Indels 49; Gaps 11;

12 GVAADTSLRSITTPQMEK-----ANGETAYLPCRFITLGPEDQPLDIEMWLSPADNQ 65

Db 3543 GPOECFAKIVLEPAVIEKPEPVAVTADGSCSTLECYDGTPE-----LTAR----- 3590

12 GVAADTSLRSITTPQMEK-----ANGETAYLPCRFITLGPEDQPLDIEMWLSPADNQ 65

Db 3543 GPOECFAKIVLEPAVIEKPEPVAVTADGSCSTLECYDGTPE-----LTAR----- 3590

3543 GPOECFAKIVLEPAVIEKPEPVAVTADGSCSTLECYDGTPE-----LTAR----- 3590

3543 GPOECFAKIVLEPAVIEKPEPVAVTADGSCSTLECYDGTPE-----LTAR----- 3590

3543 GPOECFAKIVLEPAVIEKPEPVAVTADGSCSTLECYDGTPE-----LTAR----- 3590

3543 GPOECFAKIVLEPAVIEKPEPVAVTADGSCSTLECYDGTPE-----LTAR----- 3590

3543 GPOECFAKIVLEPAVIEKPEPVAVTADGSCSTLECYDGTPE-----LTAR----- 3590

3543 GPOECFAKIVLEPAVIEKPEPVAVTADGSCSTLECYDGTPE-----LTAR----- 3590

3543 GPOECFAKIVLEPAVIEKPEPVAVTADGSCSTLECYDGTPE-----LTAR----- 3590

3543 GPOECFAKIVLEPAVIEKPEPVAVTADGSCSTLECYDGTPE-----LTAR----- 3590

3543 GPOECFAKIVLEPAVIEKPEPVAVTADGSCSTLECYDGTPE-----LTAR----- 3590

3543 GPOECFAKIVLEPAVIEKPEPVAVTADGSCSTLECYDGTPE-----LTAR----- 3590

3543 GPOECFAKIVLEPAVIEKPEPVAVTADGSCSTLECYDGTPE-----LTAR----- 3590

RESULT 5
T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20992; T24733
R:Sulston, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19355
A:Accession: T20992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5175 <MI>
A:Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a
A:Experimental source: clone F15G9
R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
Reference number: Z19929
Accession: T24733
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5175 <MI>
A:Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A:Experimental source: clone T09B9
C:Genetics:
A:Gene: CESP:F15G9.4a
A:Map position: X
A:Intons: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
1; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1;
Query Match 8.4%; Score 159; DB 2; Length 5175;
Best Local Similarity 25.4%; Pred. No. 0.015;
Matches 68; Conservative 32; Mismatches 92; Indels 76; Gaps 12;
OY 12 GVAIDLTRSLSTTPEQIE-----KAKGETAVLPFCFTLGPPEGGLDIEMWLSPPADNQ 65
DB 3845 GVALEKLVLDVFTPPVSVKSDNPDKALGETTLFCNAGSNPYQ-----LKW----- 3892
OY 66 KVDQVILYSGDKIYD---YYODLGRVHFTSNDLKGASINVTNMLQSLDITGYOCKV 122
DB 3893 -----AKGSLIFDPPDGRISLKG-----ARDDIPLKKTVDYDTCQA 3932
OY 123 KKAPEGNNKKIQLTVLKPSTGRCYVDGSEIEGDFKCEPKEGSLPLYEWOKLSNSQ 182
OY 3933 LMAAGTSEASVSDVLPPEINRDGIDMSPL-----PAQOSLTL-----OCLAQK 3979
OY 183 KLPLTL-WLAEMT-----SPVISYKNASTEYSCTYKKNRVSQOCLRL 227
DB 3980 PVPQMRWTLNGTALHTSTPGITVASDSTFTQIINNVSLSKGVYTCYAEVNAAGSDNLMYNV 4039
OY 228 DVV--PPSNRAGT---TAG--AVIGVLL 248
DB 4040 DVQAPVTSNGGTQVIEGELAVIECLV 4067
RESULT 6
T43290
hemicleitin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C:Accession: T43290; T20993; T24734
R:Yogel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A:Description: Hemicleitin is required for hemidesmosome mediated cell adhesion and germ
A:Reference number: Z22396
A:Accession: T43290
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5198 <VOG>

A:Cross-references: EMBL:AF074901; PIDN:AAC26792.1
R:Sulston, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19355
A:Accession: T20993
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5198 <MI>
A:Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
A:Experimental source: clone F15G9
R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
Accession: T24734
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5198 <MI>
A:Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
A:Experimental source: clone T09B9
C:Genetics:
A:Gene: him-4; F15G9.4b
A:Map position: X
A:Intons: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184
1; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 303
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 51
Query Match 8.4%; Score 159; DB 2; Length 5198;
Best Local Similarity 25.4%; Pred. No. 0.015;
Matches 68; Conservative 32; Mismatches 92; Indels 76; Gaps 12;
OY 12 GVAIDLTRSLSTTPEQIE-----KAKGETAVLPFCFTLGPPEGGLDIEMWLSPPADNQ 65
DB 3845 GVALEKLVLDVFTPPVSVKSDNPDKALGETTLFCNAGSNPYQ-----LKW----- 3892
OY 66 KVDQVILYSGDKIYD---YYODLGRVHFTSNDLKGASINVTNMLQSLDITGYOCKV 122
DB 3893 -----AKGSLIFDPPDGRISLKG-----ARDDIPLKKTVDYDTCQA 3932
OY 123 KKAPEGNNKKIQLTVLKPSTGRCYVDGSEIEGDFKCEPKEGSLPLYEWOKLSNSQ 182
OY 3933 LMAAGTSEASVSDVLPPEINRDGIDMSPL-----PAQOSLTL-----OCLAQK 3979
OY 183 KLPLTL-WLAEMT-----SPVISYKNASTEYSCTYKKNRVSQOCLRL 227
DB 3980 PVPQMRWTLNGTALHTSTPGITVASDSTFTQIINNVSLSKGVYTCYAEVNAAGSDNLMYNV 4039
OY 228 DVV--PPSNRAGT---TAG--AVIGVLL 248
DB 4040 DVQAPVTSNGGTQVIEGELAVIECLV 4067
RESULT 7
I49503
B-lymphocyte activation antigen 7 precursor - mouse
N:Alternate names: MB7-2
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C:Accession: I49503; S17291; I49521
R:Selvakumar, A.; White, P.C.; Dupont, B.
Immunogenetics 38, 292-295, 1993
A:Title: Genomic organization of the murine B-lymphocyte activation antigen B7.
A:Reference number: I49503; MUID:93307789
A:Accession: I49503
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:I49503; NID:q293299; PIDN:AAA37240.1; PID:q293301
R:Freeman, G.J.; Gray, G.S.; Gimm, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Finge
J. Exp. Med. 174, 625-631, 1991
A:Title: Structure, expression, and T cell costimulatory activity of the murine homol
A:Reference number: S17291; MUID:91341422
A:Accession: S17291

A:Molecule type: mRNA
 A:Residues: 1-274, 'R', 279-309 <PRE>
 A:Cross-references: EMBL:X60958; NID:950111; PIDN:CAA43291.1; PID:950112
 R:Biochem. M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Ueda, T.
 Biochem. Biophys. Res. Commun. 200. 443-449, 1994
 A:Title: Identification of an alternatively spliced form of the murine homologue of B7.
 A:Reference number: 149521; MUID:94220123
 A:Accession: 149521
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-143, 238-274, 'R', 279-309 <RE2>
 A:Cross-references: GB:D16220; NID:9505118; PIDN:BA03748.1; PID:9994769
 A:Gene: B7
 A:Introns: 37/1; 143/1; 237/1; 275/1
 C:Superfamily: B-lymphocyte restricted antigen B7
 C:Keywords: alternative splicing

Query Match 8.3%; Score 157.5; DB 2; Length 309;
 Best Local Similarity 22.0%; Pred. No. 0.00056;
 Matches 67; Conservative 61; Mismatches 116; Indels 61; Gaps 14;

```

OY 3 LLLCVLLCGVADLTRSLSTTPPEOMIEKAGETAVLPGRFTLGPEDGPDLEMLLSRA 62
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
DB 21 LLLVLLVLRISQVSSDV-----DEQLSKSVKDKVLLPCRYNPSHDESEDRYW----- 70

OY 63 DNQKVDQVLI-LYSGD-KIYDDYODLKGHVFTSNDLKSQDASINVTNQLSDIGTYOC 120
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
DB 71 --QKHDKVLVSIAGKAKWMPY-----KNRTLYDMTTY-----SLILGLVLSDRGTYS 119

OY 121 KKKKAPGCKNKIKQLTVLKPS-----GTRCYVDSGSEETGDNFKLCEPKESLPLEYEW 175
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
DB 120 VQOKER-GTYEVKHALATVLSIKADFSPTNTEGNSPADRKRTCFASGGEPPKPRFSW 178

OY 176 OKLSNOKPTLMLAEMTSPVSVKNAST--EYSGYSCCTVKNRVSQDCLRL----- 227
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
DB 179 --LENGRELPGINTITISQPESELYTISQDLPNTNRNTIK-----CLKYGDAAHS 229

OY 228 -----DVPVPSNRAGTIAGAVIGVLLALVGLIV--FCCHKR-----REKEYEKE 272
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
DB 230 EDFTEKPEDEPPDSKNTLVLFAGAGVAVTVVIVIIKCFCKHNLQSCCFRRNEASRE 289

OY 273 VHHDI 277
    : : : : :
DB 290 TNNSL 294
```

RESULT 8
 093
 A:R2 delta - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
 C:Accession: 168093
 R:Eberley, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
 Gene 159. 267-272, 1995
 A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
 A:Reference number: 153960; MUID:95347610
 A:Accession: 168093
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-538 <RES>
 A:Cross-references: GB:S79172; NID:91042204; PID:91042205
 A:Gene: PRR2delta
 C:Superfamily: poliovirus receptor; immunoglobulin homology
 F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 8.0%; Score 152.5; DB 2; Length 538;
 Best Local Similarity 23.7%; Pred. No. 0.0026;
 Matches 86; Conservative 51; Mismatches 155; Indels 71; Gaps 17;

```

OY 27 OMIEKAGETAVLPGRFTLGP-----EDQGPLDIEMLSPADNOKVDQVITLNSGD 77
    : : : : : : : : : : : : : : : : : : : : : : : : :
DB 157 RIAKPKNOAEQKVTFEQDPTVALCSKGRPPARISMSLDWEAKETOV-----SG- 211

OY 78 KIYDDYODLNGRVHFTSND--LKSQDASINVTNQLSDIGYOCKV-----KAPGVNK 131
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
DB 212 -----TLGTVTVIRFTLVPSGRA-----DGYTVCKVHESFEPPAL--I 251

OY 132 KIQLTVLLKPSGTRCYVDSGEIEG--NDFKLCEPKESGPLIYEMOKLSNOKPTLMLA 190
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : :
DB 252 PVTLSVRPPEVSIISGYDDNMTLGRDTATLSDVANSNEPIGYDMSTSGF--PPTSAYA 309

OY 191 EMTSPVSVKNASTEYSGTCTYKKNRVSGDCLRLDYVPPSNAGT-----IAGAVIG 245
    : : : : : : : : : : : : : : : : : : : : : : : : :
DB 310 QGSQLVIAH--VDSLFTNTFTVCTVNAVGMKRAEQVIFVRETPNTAGAGATGIIIGIIA 367

OY 246 VLLALVILGLIVFCCHKRREKEYEKEVHHIDREDVP--PPKSRTPARSVLSGNSHSL 302
    : : : : : : : : : : : : : : : : : : : : : : : : :
DB 368 AIIATVAVATGILICRQKREOTLQGAEDDELEPPSYKPTPKAKLEADMPSQLFTL 427

OY 303 GSMSPSNMEGYSKTOY-----NQVPSDEFERAPQSPPL-----PLAKVAPNLSRMGAVPV 353
    : : : : : : : : : : : : : : : : : : : : : : : : :
DB 428 GASEHSPL-----KTPYFDAGASCTEQEMPVRYHELPTLEERSOPL-----HPGATSLGS-PI 478

OY 354 MTP 356
    : : : : :
DB 479 PVP 481
```

RESULT 9
 A:2164
 bilinary glycoprotein 1 precursor, splice form a - human
 N:Alternate names: transmembrane carcinoembryonic antigen 1 (Tm1-CEA); transmembrane
 N:Contents: bilinary glycoprotein 1, splice form b; bilinary glycoprotein 1, splice for
 C:Species: Homo sapiens (man)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: A32164; B30127; A48078; S45664; S65939; A30847; G44476
 R:Rhioda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Heft
 Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989
 A:Reference number: A94206; MUID:88320555
 A:Contents: annotation
 A>Note: The sequence shown in this reference has been completely corrected in referen
 R:Barrett, T.R.; Kretschnier, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Eiting, J.T.
 J. Cell Biol. 108, 267-276, 1989
 A:Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mR
 A:Reference number: A92752; MUID:89139550
 A:Accession: A30127
 A:Molecule type: mRNA
 A:Residues: 1-526 <HIN>
 A:Cross-references: GB:J03858; NID:9179439; PIDN:AAA51826.1; PID:9179440
 R:Rhioda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Heft
 Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988
 A:Title: Molecular cloning of a cDNA coding bilinary glycoprotein I: Primary structure
 A:Reference number: A94206; MUID:88320555
 A:Contents: annotation
 A>Note: The sequence shown in this reference has been completely corrected in referen
 R:Barrett, T.R.; Kretschnier, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Eiting, J.T.
 J. Cell Biol. 108, 267-276, 1989
 A:Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mR
 A:Reference number: A92752; MUID:89139550
 A:Accession: A30127
 A:Molecule type: mRNA
 A:Residues: 1-526 <BARI>
 A:Cross-references: EMBL:X16354; NID:937197; PIDN:CAA4404.1; PID:937198; EMBL:X14784
 A:Experimental source: splice form a
 A:Accession: B30127
 A:Molecule type: mRNA
 A:Residues: 1-319, 'D', 417-526 <BAR2>
 A:Cross-references: EMBL:X14831; NID:937199; PIDN:CAA32940.1; PID:937200; EMBL:X14784
 A:Experimental source: splice form b
 R:Barrett, T.R.; Drake, L.; Pickle II, W.
 Mol. Cell. Biol. 13, 1273-1282, 1993
 A:Title: Human bilinary glycoprotein gene: characterization of a family of novel alter
 A:Reference number: A48078; MUID:93140765
 A:Accession: A48078
 A:Molecule type: mRNA
 A:Residues: 124-141, 'H', 417-526 <BAR3>
 A:Cross-references: GB:M76742; NID:9179480; PIDN:AAA57142.1; PID:9179481

A: Experimental source: splice form x
 A: Note: sequence extracted from NCBI backbone (NCBIN:123602, NCBIPI:123606)
 A: Note: neither the complete nucleic acid sequence nor the complete translation are shown
 R: Hauck, W.; Nedellic, P.; Turbide, C.; Stanners, C.P.; Barnett, T.R.; Beauchemin, N.
 Eur. J. Biochem. 223, 529-541, 1994
 A: Title: Transcriptional control of the human biliary glycoprotein gene, a CEA gene family
 A: Reference number: S45664; MUID: 9433343
 A: Accession: S45664
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-21 <HND>
 A: Cross-references: EMBL: X67277; NID: g29447; PIDN: CAA47694.1; PID: g606777
 R: Nedellic, P.; Turbide, C.; Beauchemin, N.
 Eur. J. Biochem. 231, 104-114, 1995
 A: Title: Characterization and transcriptional activity of the mouse biliary glycoprotein
 A: Reference number: S65939; MUID: 95354678
 A: Accession: S65939
 A: Status: preliminary; translation not shown
 A: Molecule type: DNA
 A: Residues: 1-21 <NED>
 A: Cross-references: EMBL: X67277; NID: g29447; PIDN: CAA47694.1; PID: g606777
 A: Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
 A: Note: only a part of the coding sequence is given
 R: Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
 Genomics 14, 384-390, 1992
 A: Title: Identification of three new genes and estimation of the size of the carcinoembryonic antigen precursor amino-terminal homology
 A: Reference number: A44476; MUID: 93052339
 A: Contents: annotation; alignment of related sequences
 A: Genetics:
 A: Gene: GDB: BCP
 A: Cross-references: GDB: 127992; OMIM: 109770
 A: Map position: 19q13.2-19q13.2
 C: Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal homology
 C: Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein
 F: 1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
 F: 1-34/Domain: signal sequence #status predicted <SIG>
 F: 35-526/Product: biliary glycoprotein 1, splice form a #status predicted <MATA>
 F: 35-428/Domain: extracellular #status predicted <EXT>
 F: 35-319, 'D', 417-526/Product: biliary glycoprotein 1, splice form b #status predicted <MATA>
 F: 35-111, 'H', 417-526/Product: biliary glycoprotein 1, splice form x #status predicted <MATA>
 F: 160-217/Domain: immunoglobulin homology <IM1>
 F: 252-301/Domain: immunoglobulin homology <IM2>
 F: 341-398/Domain: immunoglobulin homology <IM3>
 F: 425-454/Domain: transmembrane #status predicted <TM>
 F: 453-526/Domain: intracellular #status predicted <INT>
 F: 104, 111, 115, 152, 182, 197, 208, 224, 232, 254, 274, 288, 292, 302, 309, 345, 351, 363, 378, 405, 475/BI

Query Match 8.0%; Score 151; DB 1; Length 526;
 Best local similarity 22.4%; Pred. No. 0.0032;
 Matches 76; Conservative 56; Mismatches 133; Indels 74; Gaps 18;

QY 49 DQGLDIEMLSPADNOKVQVY--ILYSGD---KTYDYQ--DLKGVHTSN--- 96
 DB 209 DTGYECE-IQNPYSANRSPVLTNVTGPDTPRTISPSDYRRGAMLSQVYASNP 267
 QY 97 -----DLKSGDASINVTNLOLSDIGTQCKKAPGVGNKKIQTLVLL-----K 140
 DB 268 QYSLINGTQOOSTQELFRITVYNNSGSTTCANNSVTGCKRTVTTITTELSPVYAK 327
 QY 141 P--SGTRCYVDGSEIIGNDFKLCEPREGSLPL--LYEMOKLSQKPLPTLMLAEMTSPV 196
 DB 328 PQKASKRTVYTGDKDSVN--LTCSTNDTGISIMWFKNQSPLSEHMK-----LSQGNNT 380
 QY 197 ISYKNASTESGTYSCYVKNRVG---SDQCLRL--DVPSPSN--RAGTAGAVIGV--L 247
 DB 381 LSTNPVREDAGTYWCVFNPISKNSQSPITMLNVTNALPQENLSCGALAGIYGVALL 440
 QY 248 LALVLIQLIYFCCHRRREKREYVHHDIREDPVPPKSRSTARSYLGSHSLSGMSMP 307
 DB 441 VALIAVALAFLHRTGKGRASDQR-----DLTEHKPSV-----SNHTDDHSDNP 484
 QY 308 SNMEGYSKTOYNOVPSDEFERAPDSPTPLAKVAPMLIS 346

DB 485 PN-----KMEVYSTLNFEAQOPROPS--ASPSLT 514
 RESULT 10
 I38346
 elastic titin - human (fragment)
 C: Species: Homo sapiens (man)
 C: Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
 C: Accession: I38346
 R: Label: S.; Kolmerer, B.
 Science 270, 293-296, 1995
 A: Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
 A: Reference number: A57430; MUID: 96026330
 A: Accession: I38346
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: mRNA
 A: Residues: 1-7962 <RES>
 A: Cross-references: EMBL: X90569; NID: g1017426; PIDN: CAA62189.1; PID: g1017427
 C: Genetics:
 A: Gene: GDB: TTN
 A: Cross-references: GDB: 127867; OMIM: 188840
 A: Map position: 2q31.2q31

Query Match 8.0%; Score 151; DB 2; Length 7962;
 Best local similarity 23.9%; Pred. No. 0.099;
 Matches 61; Conservative 31; Mismatches 77; Indels 86; Gaps 12;

QY 12 GVADLTRSLSTTP-----EQMTEKAKGETAVLPCRFITLPEPDG--PLDIEMLSPAD 63
 DB 4050 GSASSSTSLKWKKEPRFRKKPHETLKGADVHLEC-----ELQGRPFHVSW----- 4097
 QY 64 NQKDYVYIILSGKITDYQDLKGVHFTSNLKSQD-----ASINTNQLS 113
 DB 4098 -----YKD-----KRLRSQKTKYKXSENFVLSIHILNDAA 4129
 QY 114 DIGTYQCKVKKAPGVGNKKIQTLVLLK--PSGTRCYVDGSEIIGNDFKLCEPREGSLPL 171
 DB 4130 DIGTYQCKATN--DVSGDTCVGSIALKAPRFVAKKLDSIVGKRVQQLQ--TTIEGAEPI 4186
 QY 172 LYEMOK-----LSNSQKPLPTLAEHTSPVSYVKNASTESGTYSCYVKNRV 218
 DB 4187 SVVWFKKGEIVRSDINWISYENIATLOFSR-----VEPANA-----GKVTQIRKDA 4236
 QY 219 GSDQCLRLDVPVPS 233
 DB 4237 GMDCEFAFLVLEPA 4251

RESULT 11
 JC4024
 poliovirus receptor-related protein precursor - human
 C: Species: Homo sapiens (man)
 C: Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
 C: Accession: JC4024
 R: Lopez, M.; Eberle, F.; Mattel, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maro, C.; D
 Gene 155, 261-265, 1995
 A: Title: Complementary DNA characterization and chromosomal localization of a human g
 A: Reference number: JC4024; MUID: 95237621
 A: Accession: JC4024
 A: Molecule type: mRNA
 A: Residues: 1-518 <LOP>
 A: Cross-references: EMBL: X76400; NID: g732795; PIDN: CAA53980.1; PID: g732796
 C: Genetics:
 A: Gene: GDB: PVRL1
 A: Cross-references: GDB: 583951
 A: Map position: 11q23.11q24
 C: Superfamily: poliovirus receptor; immunoglobulin homology
 C: Keywords: glycoprotein; transmembrane protein
 F: 1-30/Domain: signal sequence #status predicted <SIG>
 F: 31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
 F: 356-379/Domain: transmembrane #status predicted <TM>

R:lin, S.H.; Guidotti, G.
J. Biol. Chem. 264, 14408-14414, 1989
A:Title: Cloning and expression of a cDNA coding for a rat liver plasma membrane ecto-AT
A:Reference number: A44783; MUID:89340561
A:Accession: A44783
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-519 <LIN>
A:Cross-references: GB:J04963; NID:g203989; PID:AAA41104.1; PID:g203990
R:Stippel, C.J.; Suchy, F.J.; Ananthanarayanan, M.; Perlmuter, D.H.
J. Biol. Chem. 268, 2083-2091, 1993
A:Title: The rat liver ecto-ATPase is also a canalicular bile acid transport protein.
A:Reference number: A44410; MUID:93131966
A:Accession: A44410
A:Molecule type: protein
A:Residues: 110-120;122-138;148-150 <STP>
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C:Keywords: glycoprotein; liver; phosphoprotein; transmembrane protein
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:160-217/Domain: immunoglobulin homology <IMM1>
F:252-301/Domain: immunoglobulin homology <IMM2>
F:337-394/Domain: immunoglobulin homology <IMM3>

Query Match 7.7%; Score 146.5; DB 2; Length 519;
Best Local Similarity 21.3%; Pred. No. 0.0066;
Matches 74; Conservative 58; Mismatches 136; Indels 79; Gaps 18;
QY 28 MIEAKGETAVLPCR---FTLGPEDGRLDIEM---LISPADNQKVDVYIILYSGDK 78
Db 202 LLNVRDQKGYECEARNPATEFNRSDEPNLDVYGPDAVPISPPD-----IYHQGSN 254
QY 79 IYDDYODLKGVRHF---TSNDLKSQDASIMVNTNLSIDIGYOCKVKK-APVGNKKIO 134
Db 255 LNLSCHADSNPPAQFYMLINEKLOTSSQELISNTITNSGTACFVNTYTGLSRTIVK 314
QY 135 LTVLKPSTGRCYVDGSEIEGN-----DFLKPCEKESLPPLYEMOKLSNOKLPTL 187
Db 315 NITVEEP-----VTPQSIQINTVYKELGSVTLICFSGKDTGVSV--RW--LFNSQSL--- 362
QY 188 WLAETSTVIVYKNAST-----EYSGTSCIVYKN---RVGSDQCLRLDVYPPSPNR 235
Db 363 ---OLTDMLTSDONSTLRIDPIKREDAGDYQCEISNPVSFRISHP---IKLDVTPDPTQ 416
QY 236 A-----CTIAGAVIYGLVLAIVGLIYECCHKKREKYEKVEVHHDIRVDVPPKSTS 289
Db 417 GNSGLSEGAIGIYIGSYAGVALLAALAYFLYKRTGGGSD---HRDLTEKRP-----S 467
Db 290 TARSTLGSNHSLSGMSPSNME--GYSKTYQNVPSDEDFERAPQSPPT 334
468 TSSNHLGSPD-----SPNKVDVSYSLNFMNAOOSKRPSTASSSPT 509

RESULT 15
JC5288
SHP substrate-1 protein, 509 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C:Accession: JC5288
R:Yamao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioaka, Y.;
Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A:Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization
A:Reference number: JC5287; MUID:97223399
A:Contents: Brain
A:Accession: JC5288
A:Molecule type: mRNA
A:Residues: 1-509 <YAM>
A:Cross-references: DDBJ:D87967; NID:91864012; PIDN:BA13520.1; PID:91864013
C:Comment: This protein is a glycosylated receptor-like protein and plays a role in cell
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
C:Genetics:
A:Gene: shps-1
A:Map position: 2

Query Match 7.7%; Score 145.5; DB 2; Length 509;
Best Local Similarity 19.4%; Pred. No. 0.0076;
Matches 103; Conservative 69; Mismatches 151; Indels 207; Gaps 23;
QY 3 LLLCFVL--LCGVADLT--RSLITTPPEOMIEKAGETAVLPCRFT---LGPEDGRLDI 55
Db 14 LLLCLLSASCFGCVGTCKELKLVQPEKSVAGADSTVLMCTLSLPLVGP-----I 66
QY 56 EMLSPADNQKVDVYIILYSGDKIYDDYODLKGVRHFTSNDLKS--DASIMVNTNLS 113
Db 67 KMYRGVQGR-----LLIYS-----FTGHPFPRVTWSDATKRNMDFSIRISNTVPE 114
QY 114 DIGTYQC-KVKKAPGVGNKKIO-----LTVLLKPSGRCYVDGSEIEG---NDEKLKE 163
Db 115 DAGTYCVKFGKGPSEPTETIQSGGTEVYVLAKEPSPE--VSGPADKIPDQKYNFTCK 172
QY 164 ---PKGSLPLYEMOKLS-----NSOKLPTLMAEM- 192
Db 173 SHGSPRNTITLKWFGDGLHLETTVNPSSGKNVSNISSTVRYVLNMDVHAKYICVA 232
QY 193 -----TSPVISTV----- 199
Db 233 HTLDRSPLRGIANLNFIRVSPVYKYOQSPSTSMNOVNLTCRAEFYEDLQILMLENG 292
QY 200 -----KNASTEYSGTSCIVKNRVGS-----QCLLRDVPSPNRAGTIAGAV 243
Db 293 NVSRNDTPKRLTKNTDGYVNTSLFLVNSAAREDEVFTCOVKHDQOATIRNHTVLGLA 352
QY 244 -----IGVLLALVLIGLI--VECCHKRRKRE----- 266
Db 353 HSSDQSMQTEPPGNATNNMNVFIVGVACALLVLLMAALYLILIKKKKKSGSTSRRL 412
QY 267 ---EKYEKV-----HHDIR-----DVPPKSPSTANSTYSGNHSLSGMSPSNMEYS 314
Db 413 HEPEKNAREITQIDPTNDINDITYADLNLPEKKPAPRAPAPENNTE-----YA 461
QY 315 KTOYNVPSDEDFERAPQSPPTLPLAKVAAPNLSRMGAVVPMIPAOSSQSI 364
Db 462 SIETGKVRPE-----DTLLTYADLDMVHLISRAOPAPKPPSPSEVASV 504

Search completed: May 11, 2002, 13:48:36
Job time: 3593 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 2002, 12:26:48 ; Search time 28.1 Seconds
(without alignments)
317.272 Million cell updates/sec

Title: US-09-899-634A-4
Perfect score: 1898
Sequence: 1 MALLICEVLGCVADLTRSL.....SRMGAVPMIPDQSKDGSIV 365

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1754	92.4	365	US-08-979-424-3	Sequence 3, Appl
2	1754	92.4	365	US-09-272-496-2	Sequence 2, Appl
3	1740	91.7	365	US-08-928-383B-2	Sequence 2, Appl
4	1740	91.7	365	US-08-928-383B-23	Sequence 23, Appl
5	1739	91.6	365	US-08-928-383B-26	Sequence 26, Appl
6	1661	87.5	365	US-08-928-383B-24	Sequence 24, Appl
7	523	27.6	106	US-08-928-383B-8	Sequence 8, Appl
8	453	23.9	95	US-08-928-383B-17	Sequence 17, Appl
9	368.5	19.4	319	US-08-974-95B-22	Sequence 22, Appl
10	368.5	19.4	319	US-09-068-051A-22	Sequence 22, Appl
11	330.5	17.4	318	US-09-068-051A-32	Sequence 32, Appl
12	325.5	17.1	390	US-08-979-424-1	Sequence 1, Appl
13	276	14.5	387	US-09-175-928-2	Sequence 2, Appl
14	197	10.4	299	US-09-188-930-331	Sequence 331, App
15	197	10.4	299	US-09-462-270-2	Sequence 2, Appl
16	192	10.1	299	US-09-188-930-189	Sequence 189, App
17	164.5	8.7	1101	US-08-986-485-2	Sequence 2, Appl
18	163.5	8.6	269	US-09-430-503-6	Sequence 6, Appl
19	163.5	8.6	269	US-09-430-503-8	Sequence 8, Appl
20	161.5	8.5	269	US-09-430-503-4	Sequence 4, Appl
21	161.5	8.5	306	US-08-205-697A-17	Sequence 17, Appl
22	161.5	8.5	306	US-08-702-525-17	Sequence 17, Appl
23	161.5	8.5	306	PCT-US95-02576-17	Sequence 17, Appl
24	160.5	8.5	1091	US-08-986-485-5	Sequence 5, Appl
25	159.5	8.4	269	US-09-430-503-2	Sequence 2, Appl
26	158.5	8.4	306	US-08-147-772-4	Sequence 4, Appl
27	158.5	8.4	306	US-08-456-104-8	Sequence 8, Appl

28	158.5	8.4	306	US-08-101-624-25	Sequence 25, Appl
29	158.5	8.4	306	US-08-153-262-4	Sequence 4, Appl
30	158.5	8.4	306	US-08-479-744A-31	Sequence 31, Appl
31	158.5	8.4	306	US-08-280-757B-31	Sequence 31, Appl
32	158.5	8.4	306	US-09-159-135-4	Sequence 4, Appl
33	158.5	8.4	306	US-09-450-798-4	Sequence 4, Appl
34	158	8.3	209	US-09-430-503-20	Sequence 20, Appl
35	158	8.3	209	US-09-430-503-24	Sequence 24, Appl
36	156	8.2	209	US-09-430-503-18	Sequence 18, Appl
37	156	8.2	209	US-09-430-503-22	Sequence 22, Appl
38	154.5	8.1	320	US-08-205-697A-2	Sequence 2, Appl
39	154.5	8.1	320	US-08-702-525-2	Sequence 2, Appl
40	154.5	8.1	320	PCT-US95-02576-2	Sequence 2, Appl
41	152.5	8.0	581	US-08-724-394A-3	Sequence 3, Appl
42	145.5	7.7	581	US-08-724-394A-2	Sequence 2, Appl
43	145	7.6	205	US-09-462-270-4	Sequence 4, Appl
44	143	7.5	199	US-09-430-503-44	Sequence 44, Appl
45	143	7.5	199	US-09-430-503-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-08-979-424-3
; Sequence 3, Application US/08979424
; Patent No. 5942606
; GENERAL INFORMATION:
; APPLICANT: Lal, Preethi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,424
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0405 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 1946351
; US-08-979-424-3

Query Match 92.4%; Score 1754; DB 2; Length 365;
Best Local Similarity 90.7%; Pred. No. 2,5e-155;

	Matches	331:	Conservative	16:	Mismatches	18:	Indels	0:	Gaps	0:
OY	1	MALLICFVLLCGVADLT	RSLSITTTBEOMIERAKG	EATYLPCKFTLGEPOG	PLDIEMLLS	60				
Db	1	MALLICFVLLCGVADV	FARSLSTTPEEMIEKAKG	EATYLPCKFTLGEPOG	PLDIEMLLS	60				
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Db	61	PADNOKVQOVIILLY	SGDKYYDDYODD	IKGRVAFTSNDLKS	SGASINWTMLQSD	ISTGYOC	120			
OY	121	KVKKAPGVGNKKIOL	TVLLKPSGTRCYVD	SGEIGNDFLKCEPK	EGSLPILLEY	EWOKLSN	180			
Db	121	KVKKAPGVGNKKIOL	TVLLKPSGTRCYVD	SGEIGNDFLKCEPK	EGSLPILLEY	EWOKLSN	180			
OY	181	SGKLTPLMLAEMTS	SPYISYKKNASTE	SGSYCTSVCKNRV	SDOCLRLDVP	PPSNRAGTIA	240			
Db	181	SGKLTPLMLAEMTS	SPYISYKKNASTE	SGSYCTSVCKNRV	SDOCLRLDVP	PPSNRAGTIA	240			
OY	241	GAVIEVLLALTVL	IGLIVFCCHKKR	REEREKEVE	HHNIDREDVP	PPKRSRTAST	SYLSGNS	300		
Db	241	GAVIEVLLALTVL	IGLIVFCCHKKR	REEREKEVE	HHNIDREDVP	PPKRSRTAST	SYLSGNS	300		
OY	301	SLGSMSPSMMEGY	SKTOYNQVPS	SEDFERAPQ	SPTLPLAKVA	APNLSRMGA	VPVMI	PAQSK	360	
Db	301	SLGSMSPSMMEGY	SKTOYNQVPS	SEDFERAPQ	SPTLPLAKVA	APNLSRMGA	VPVMI	PAQSK	360	
OY	361	DGSIIV	365							
Db	361	DGSIIV	365							

RESULT 2
 US-09-272-496-2
 : Sequence 2, Application US/09272496
 : Patent No. 6245966
 : GENERAL INFORMATION:
 : APPLICANT: Degregori, James
 : TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
 : FILE REFERENCE: 90-98
 : CURRENT APPLICATION NUMBER: US/09/272,496
 : CURRENT FILING DATE: 1999-03-19
 : EARLIER APPLICATION NUMBER: US 60/092782
 : EARLIER FILING DATE: 1998-07-14
 : NUMBER OF SEQ ID NOS: 7
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 2
 : LENGTH: 365
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : 09-272-496-2

Query Match	92.4%	Score 1754	DB 4	Length 365
Best Local Similarity	90.7%	Pred No. 2.5e-155		
Matches 331; Conservative	16	Mismatches 18	Indels 0	Gaps 0

[illegible]

Accession	Sequence	Length
Dd	241 GAIOTLLALIGLIIFCCRRKRREKEVEVHNDIEDVPPPKSTSTARSYSIGSNHS	300
Qy	301 SLGSMSPENMGYSKTYQNOVPSDFEFAPOSPFLPLAKAAAPLSSMGAVPVVPIAOSK	360
Dd	301 SLGSMSPENMGYSKTYQNOVPSDFEFTPTQSPFLPAKAAAPLSSMGAVPVVPIAOSK	360
Qy	361 DGSIV 365 	
Dd	361 DGSIV 365	

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1 RESULT 3
2 US-08-928-383B-2
3 : Sequence 2, Application US/08928383B
4 : Patent No. 6210921
5 :
6 : GENERAL INFORMATION:
7 :
8 : APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
9 : Applicant: and Marshall S. Horwitz
10 :
11 : TITLE OF INVENTION: CAR, A No. 6210921el Cxsacklevirus and Adenovirus
12 :
13 : TITLE OF INVENTION: Receptor
14 :
15 : NUMBER OF SEQUENCES: 26
16 :
17 : CORRESPONDENCE ADDRESSES:
18 :
19 : ADDRESSEE: LAHIVE & COCKFIELD, LLP
20 :
21 : STREET: 28 State Street
22 :
23 : CITY: Boston
24 :
25 : STATE: Massachusetts
26 :
27 : COUNTRY: USA
28 :
29 : ZIP: 02109
30 :
31 : COMPUTER READABLE FORM:
32 :
33 : MEDIUM TYPE: Floppy disk
34 :
35 : COMPUTER: IBM PC compatible
36 :
37 : OPERATING SYSTEM: PC-DOS/MS-DOS
38 :
39 : SOFTWARE: Patentln Release #1.0, Version #1.25
40 :
41 : CURRENT APPLICATION DATA:
42 :
43 : APPLICATION NUMBER: US/08/928,383B
44 :
45 : FILING DATE: 12-SEP-1997
46 :
47 : CLASSIFICATION:
48 :
49 : PRIOR APPLICATION DATA:
50 :
51 : APPLICATION NUMBER: US 60/026,100
52 :
53 : FILING DATE: 13-SEP-1996
54 :
55 : ATTORNEY/AGENT INFORMATION:
56 :
57 : NAME: Mandragouras, Amy E.
58 :
59 : REGISTRATION NUMBER: 36,207
60 :
61 : REFERENCE/DOCKET NUMBER: DFN-020
62 :
63 : TELECOMMUNICATION INFORMATION:
64 :
65 : TELEPHONE: (617)227-7400
66 :
67 : TELEFAX: (617)742-4214
68 :
69 : INFORMATION FOR SEQ ID NO: 2:
70 :
71 : SEQUENCE CHARACTERISTICS:
72 :
73 : LENGTH: 365 amino acids
74 :
75 : TYPE: amino acid
76 :
77 : TOPOLOGY: linear
78 :
79 : MOLECULE TYPE: protein
80 :
81 US-08-928-383B-2

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Query Match	Similarity	91.7%	Score 1740:	DB 4:	Length 365:
Best Local	Similarity	90.4%	Pred. No. 5.1e154:		
Matches	Conservative	16:	Mismatches	19:	Indels 0; Gaps 0;
QY	1	MALLLCFVLLCGVADLITRSLSTITTPPEOMIERAKGGETAYLPCPFITLGPEDQGPLDIEMLS	60		
Db	1	MALLLCFVLLCGVADLITRSLSTITTPPEOMIERAKGGETAYLPCPFITLGPEDQGPLDIEMLS	60		
QY	61	PADNOKVDOVILLYSGDKIYDDYIYODLKGKRVHFTSNDLKSGDASINVTNMLQSLDIGTYOC	120		
Db	61	PADNOKVDOVILLYSGDKIYDDYIYODLKGKRVHFTSNDLKSGDASINVTNMLQSLDIGTYOC	120		
QY	121	KYKKRAGVGNKKIOLITVLILKPGCTGCVYDGSFEINDEPKICEKEGSLPILLYEMOKISN	180		
Db	121	KYKKRAGVGNKKIOLITVLILKPGCTGCVYDGSFEINDEPKICEKEGSLPILLYEMOKISN	180		

Qy	181	SOKPPTLTLAMTSPVLSYKNASTSEYGGTSCATKNNVSGDOCLRLDVPSPENRAGTIA	240
Db	181	SOKMPTSSLAMTSSVLSYKNAASEYGGTSCVTRNNVSGDOCLRLNVPPSKAGLIA	240
Qy	241	GAIVGVLLAIVLIGLIYFCCHKKRREKREYKENVHDIREDVPPKSRPTSTARSYLGSNH	300
Db	241	GAIGTLLALLALIGLIIFCCCKKRREKREYKENVHDIREDVPPKSKSTSTARSYISNH	300
Qy	301	SLGSMSPSNMEGYSKTOYNVPSEDFEPAPLPLAKVAAPNLSMGAVPVMIPAQSK	360
Db	301	SLGSMSPSNMEGYSKTOYNVPSEDFEPRTDPSPLPAKVAAPNLSMGAI PVMIPAQSK	360
Qy	361	DGSTV 365	
Db	361	DGSTV 365	

RESULT 4

US-08-928-383B-23
Sequence 23, Application US/08928383B
Patent No. 6210921

GENERAL INFORMATION:

APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
APPLICANT: and Marshall S. Horwitz
TITLE OF INVENTION: CAR, A No. 6210921e1 Cocksackievirus and Adenovirus
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-928-383B-23

Query Match	91.78;	Score 1740;	DB 4;	Length 365;
Best Local Similarity	90.48;	Pred. No. 5.1e-154;		
Matches 330;	Conservative 17;	Mismatches 18;	Indels 0;	Gaps 0

OY 1 MALICFVLGVDLFRRSISITTPQEMIERAKGETAVLPORFTLGDEGGPDIIEWLS 60
| | | | | | | | | | | | | | | | | | | | | | :
Db 1 MARLLCFVLLGLIDFTSGISITTPQEIIRKAKETAYLPCKPLSPEDGGPDIIEWLS 60
| | | | | | | | | | | | | | | | | | | | | | :
OY 61 PADNQKVGVYIILTSQGIYYDYQDLKGRHFHSNDLKSSDASINTNTQLSDIGTQC 120
| : | | | | | | | | | | | | | | | | | | | | | | :
| : | | | | | | | | | | | | | | | | | | | | | | :

Db	61	PSNQIVDQVILIKVSGKIDYDNYRDLKGRVHFISNDVKSGDASINTNINQSDIGTYOC	120
QY	121	KYKAPGYGNKKIQTUTYLKPSGRICYDSDSEELGDNDFKLACEPKESLFLUYEMOKLSN	180
Db	121	KYKAPGVAANKKFLUTYLAVKPSGRICFVDDSEELGNDFKLCEPKESLFLUYEMOKLSD	180
QY	181	SQKLPPTLWLAEMTSPVLSVKNNASTEYSGTYSCTYKNNVSGDOCLRLDYVPPSNRAGTIA	240
Db	181	SQTMPTSLWLAEMTSPVLSVKNNASEYSGTYSCTYQNNVSGDOCLRLDYVPPSNRAGTIA	240
QY	241	GAVIGVILATLVLLIGLVPCCHKKRREKYEVEVHDLREVPKPKSTARSVTSNHS	300
Db	241	GAVIGTTLATLVLLIGLVPCCHKKRREKYEVEVHDLREVPKPKSTARSVTSNHS	300
QY	301	SLGMSPSNMGEYSKTOYNQVPSDFPERAPQSPPLPLAKVAAPNLSPMGAVPVVIAPOQK	360
Db	301	SLGMSPSNMGEYSKTOYNQVPSDFPERAPQSPPLTAPAKVAAPNLSPMGAVPVVIAPOQK	360
QY	361	DGSIIV 365	
Db	361	DGSIIV 365	

LT 5

US-08-928-383B-26
; Sequence 26, Application US/08928383B
; Patent No. 6210921

GENERAL INFORMATION

APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
 APPLICANT: and Marshall S. Horwitz
 TITLE OF INVENTION: CAR, A No. 6210921el Cocksacklevirus and Adenovirus
 TITLE OF INVENTION: Receptor
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/928.383B
 FILING DATE: 12-SEP-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/026.100
 FILING DATE: 13-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: DFN-020
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 365 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-928-383B-26

Query Match	91.6%;	Score 1739;	DB 4;	Length 365;
Best Local Similarity	90.4%;	Pred. No. 6.3e-154;		
Matches 330;	Conservative 17;	Mismatches 18;	Indels 0;	Gaps 0

QY 1 MALLCFVLLCGVADLTRSLSTTPPEQMIEKAKGETAYLP CRTTLGPEDGGPLDI EWLLS 60

```
Db 1 MARLLCFVLLCGIADFTSGLSITTPPEORIEKAKGETAVLPCKFTLSPEDOGPLDIEMLIS 60
Qy 61 PADNOKVOVITLYSGDITDYDODLGRVHFTSNDKSGDASINVNTLSDIGTYQC 120
Db 61 PSDNOIVQDVITLYSGDITDYDODLGRVHFTSNDKSGDASINVNTLSDIGTYQC 120
Qy 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIENDFKLCEPKESGLPLLEYMOKLSN 180
Db 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIENDFKLCEPKESGLPLLEYMOKLSN 180
Qy 181 SOKLPTLWLAETSPVIVSKNASTESGTYSCYKNNRGSQDCLRLDVPVPSNRAGTIA 240
Db 181 SOKLPTLWLAETSPVIVSKNASTESGTYSCYKNNRGSQDCLRLDVPVPSNRAGTIA 240
Qy 241 GAVIGVLLALVLLIGLIVFCCHKKRREKEYEKEVHHDIREDVPPPKSRTSTARSTYLSGNS 300
Db 241 GAVIGVLLALVLLIGLIVFCCHKKRREKEYEKEVHHDIREDVPPPKSRTSTARSTYLSGNS 300
Qy 301 SLGSMSPSNMEGYSKTYQNOVPSSEDFERAPQSPPTLPAKVAAPNLISRMGAVPVMIPAOQK 360
Db 301 SLGSMSPSNMEGYSKTYQNOVPSSEDFERAPQSPPTLPAKVAAPNLISRMGAVPVMIPAOQK 360
Qy 361 DGSIV 365
Db 361 DGSIV 365

RESULT 6
US-08-928-383B-24
; Sequence 24, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Coxsackievirus and Adenovirus
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928.383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026.100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36.207
; REFERENCE/DOCKET NUMBER: DPN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-928-383B-24
```

```
Query Match 87.5%; Score 1661; DB 4; Length 365;
Best Local Similarity 87.1%; Pred. No. 1.2e-146;
Matches 318; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

Qy 1 MARLLCFVLLCGVADLTSLSTTPPEQMIERAKGETAVLPCKFTLSPEDOGPLDIEMLIS 60
Db 1 MARLLCFVLLCGIADFTSGLSITTPPEORIEKAKGETAVLPCKFTLSPEDOGPLDIEMLIS 60
Qy 61 PADNOKVOVITLYSGDITDYDODLGRVHFTSNDKSGDASINVNTLSDIGTYQC 120
Db 61 PSDNOIVQDVITLYSGDITDYDODLGRVHFTSNDKSGDASINVNTLSDIGTYQC 120
Qy 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIENDFKLCEPKESGLPLLEYMOKLSN 180
Db 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIENDFKLCEPKESGLPLLEYMOKLSN 180
Qy 181 SOKLPTLWLAETSPVIVSKNASTESGTYSCYKNNRGSQDCLRLDVPVPSNRAGTIA 240
Db 181 SOKLPTLWLAETSPVIVSKNASTESGTYSCYKNNRGSQDCLRLDVPVPSNRAGTIA 240
Qy 241 GAVIGVLLALVLLIGLIVFCCHKKRREKEYEKEVHHDIREDVPPPKSRTSTARSTYLSGNS 300
Db 241 GAVIGVLLALVLLIGLIVFCCHKKRREKEYEKEVHHDIREDVPPPKSRTSTARSTYLSGNS 300
Qy 301 SLGSMSPSNMEGYSKTYQNOVPSSEDFERAPQSPPTLPAKVAAPNLISRMGAVPVMIPAOQK 360
Db 301 SLGSMSPSNMEGYSKTYQNOVPSSEDFERAPQSPPTLPAKVAAPNLISRMGAVPVMIPAOQK 360
Qy 361 DGSIV 365
Db 361 DGSIV 365

RESULT 7
US-08-928-383B-8
; Sequence 8, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Coxsackievirus and Adenovirus
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928.383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026.100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36.207
; REFERENCE/DOCKET NUMBER: DPN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
```


DB 239 VGIAGVAAALIIIGIITCCCCRGKNDTDEKEDARPAREVEEPPOLRELREERE 298
QY 293 -SYLGSNHSLSGMSPSNME 311
DB 299 DDYRGEQRSTGRSPDHLD 318

RESULT 10
US-09-068-051A-22

; Sequence 22, Application US/09068051A
; Patent No. 6291235

GENERAL INFORMATION:

APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
Cattmel, B.; Ji, Hong; Burgess, Anthony W.;
Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/068,051A

FILING DATE: 10-Dec-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/597,495

FILING DATE: 02-Feb-1996

APPLICATION NUMBER: 08/511,876

FILING DATE: 04-Aug-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6291235man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5316.2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3168

TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 22

SEQUENCE CHARACTERISTICS:

LENGTH: 319 amino acids

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 22

US-09-068-051A-22

Query Match 19.4%; Score 368.5; DB 4; Length 319;
Best Local Similarity 30.9%; Pred. No. 2,3e-26;
Matches 99; Conservative 62; Mismatches 128; Indels 31; Gaps 13;

QY 10 LCGVADLTSLSTTPPEQMIKAGETAYLPGRFTLGPEDGPDLEW---LLSPADNOK 66
DB 12 LCAVRTVAIVSETPQDVLASOGKSVLPCTYHTSTSSRGL-IQMDKLLLT-----H 65
QY 67 VQOVIIYSGDK--IYDDVYODLKGKRVHTSNDKSGDASINVTNQLSDIGTYOCKYK 124
DB 66 TERVVTWPNKKNYHGEIY---KNRVSI-SNNAEOSDSITIDQLTMADNGTYECSVSL 121
QY 125 ABGV-GNKK--IQLFVLPLKSGTRCYVDSEIEGNDFKLCEPKESGLPLLEYMOKLS-N 180
DB 122 MDLDEBNTSRVRLVLPVPSKPEGIEGFTIIGNNIQLTCSKESGSPFPQYSMKRYNLL 181

QY 181 SOKLPTLWLAEMTS-PVISVKNASTREYSGTSCVKNRVGSDOCLLRDVPVPSNRACGTI 239
DB 182 NOEOP---LAQPSGQPVSLKNIKSTDTSGYICTSNEBGTQFCNTIVAVRSPSNNVALY 238
QY 240 AGAVIGVLLATLVLIIGLYVCC---HKRRREKYEKEVHHDRVPPPKSTSTAR--- 292
DB 239 VGIAGVAAALIIIGIITCCCCRGKNDTDEKEDARPAREVEEPPOLRELREERE 298
QY 293 -SYLGSNHSLSGMSPSNME 311
DB 299 DDYRGEQRSTGRSPDHLD 318

RESULT 11

US-09-068-051A-32

; Sequence 32, Application US/09068051A

; Patent No. 6291235

GENERAL INFORMATION:

APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
Cattmel, B.; Ji, Hong; Burgess, Anthony W.;
Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/068,051A

FILING DATE: 10-Dec-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/597,495

FILING DATE: 02-Feb-1996

APPLICATION NUMBER: 08/511,876

FILING DATE: 04-Aug-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6291235man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5316.2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3168

TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 32

SEQUENCE CHARACTERISTICS:

LENGTH: 318 amino acids

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 32

US-09-068-051A-32

Query Match 17.4%; Score 330.5; DB 4; Length 318;
Best Local Similarity 30.0%; Pred. No. 8.1e-23;
Matches 87; Conservative 56; Mismatches 114; Indels 33; Gaps 11;

QY 9 LUCGVADLTSLSTTPPEQMIKAGETAYLPGRFTLGPEDGPDLEW---LLSPADNOK 66
DB 10 MLCALWVADALTFVETDQILRAARGSVLPCTYNTYVSDEGFIQMDKLL---RSQ 64
QY 67 VQOVII--LYSGDKIYDDVYODLKGKRVHTSNDKSGDASINVTNQLSDIGTYOCKYK 124
DB 65 TERVVTWPNFKKTYIGNRYEN---RVR-VSNDALSNASTITIDQLIMDNGTYECSVSL 120

QY 125 APGV---GNKKIQLTVLLKPSGTCYVDGSEIENDFKLCEPKESLPLIYEMOKL-SN 180
Db 121 MSODVAKRRLVLPVPPSKPCDSIOGEMVIGNNITQLCHSEGSPPSQYMSKSTINAQ 180
QY 181 SOKLPTLMLAEMTSPV---ISVKNASTEXSGTYSCYVKNRVGSDOCLLRDLVPPSPNRA 236
Db 181 NQOR-----LTQVSGEPPLLLKNISTETAGYICTSSNDVGIESCNITVAPRPSMNI 234
QY 237 GTAGANIGVLLALVIGLVFCCHKRRREKEVEVHHIDREVPPPKS 286
Db 235 ALYAGIAGSVFALLIIGVIVCCCEKREKDDOD-----REDARPNRA 278

RESULT 12
US-08-979-424-1
Sequence 1, Application US/08979424
Patent No. 5942606

GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,424
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0405 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGFET03
CLONE: 1232054
US-08-979-424-1

Query Match 17.1%; Score 325.5; DB 2; Length 390;
Best Local Similarity 27.2%; Pred. No. 3.2e-22;
Matches 111; Conservative 65; Mismatches 157; Indels 75; Gaps 16;

QY 3 LLLCEVLLCGVADLTRS-LSTTPPEOMIERAKGETAYLPCRFITLGP--DQGPLDIE-- 56
Db 13 LRFLEFLGLSALAPPSRQQLHLPLANRLQAVEGGEVLLPAMYTLHGVESSSQPWEVPEFM 72
QY 57 WLSPADNOKVDOYIIISG-----DKIYDDYODLKGRAVHTSNDLKSQDASINVT 108
Db 73 WFER--OKEREDVLSYINGVTSKPGVSLV-----SMPSRNLSTLRLE 114

QY 109 NLQSLDIGTQCKYK-----KAPVGNKKIQLTVLLKPSGTCYVDGSEIENDFKLC 162
Db 115 GLQEKDGGPIVSCSVNVDKQKSGHSTKITELVLPAPPSRCLQGVPHVGNVTLSC 174
QY 163 EPKESLPLIYEMOKLSNOKLPTLM-----LAEMTSPVSVKNASTEXSGTYSCYVKNR 217
Db 175 QSPRSKPAVOYQOMR-----QLPFGQTFEPALDLVINGSLSTLTLSSSMAGVYCKAHNE 229
QY 218 VGSQOCLLRDLVPPSNRAGTACAGVIGVLLALVIGLVFCCHKRRREKEVEVHHDI 277
Db 230 VGTQACHVTLV-VSTGGAAYVAGAVGTLGLGLAGLVLLYH--RRCALDEPANDI 285
QY 278 RED-----VPPKSRSTARSYLSGNHSLGSMSPMEGSKT-QYNQVSEDFERAP 330
Db 286 KEDAIARTRLPWPKSSDTISKNGTLSSYTSARALRPH--GPPRGALITPPLSSQALP 343
QY 331 QSPPLPLAKVAAP-----NLNRGAAPVMIIPAQSKDGSIV 365
Db 344 -SPRLPTTGDGHPQIPISPIPGVSSGSLSRMGAVPVWVPAQSQAGSLV 390

RESULT 13
US-09-175-928-2
Sequence 2, Application US/09175928A
Patent No. 6312921

GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Mi, Sha
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 60068-AJ172A
CURRENT APPLICATION NUMBER: US/09/175,928A
CURRENT FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentia Ver. 2.0
SEQ ID NO 2
LENGTH: 387
TYPE: PRT
ORGANISM: Homo sapiens
US-09-175-928-2

Query Match 14.5%; Score 276; DB 4; Length 387;
Best Local Similarity 24.9%; Pred. No. 1.3e-17;
Matches 93; Conservative 62; Mismatches 155; Indels 64; Gaps 13;

QY 7 FVLLCGVADLTRSLSTTPPEOMIERAKGETAYLPCRFITLGPEDQGPLDIEMLLSPADNOK 66
Db 9 FLILSLAGQSVYQVITPDGFVNVTVGSNVTLICITTTTVAAREQSLQ--SEFHKKE 66
QY 67 VDOYIIISY--GDKIYDDYOD-LKRAVHTSNDLKSQDASINVTNLQSLDIGTQCKYK 123
Db 67 MEPISTIYSGQGAQVAIGQEFDRITG-----SND--PGMASITISHQOPASGIYIDVN 119
QY 124 KAP---GVGNKKIQLTVLLKPSGTCYVDGSEIENDFKLCEPKESLPLIYEMOKLSN 180
Db 120 NPPFLODONGIILVNSVLPKSKPLCSVQGRPEYGHITISLCSALGTSPSYVYVHHKLEG 179
QY 181 SOKLPTLMLAEMTSPVSVKNASTEXSGTYSCYVKNRVGSDOCLLRDLVPPSNRAGTIA 240
Db 180 RDIIVKENEFPFTGLIVIGLTFNEQGYGYQCTAINRLNGSSC--EIDLTSSHPEVGLIV 237
QY 241 GAVTGVLL-ALVIGLVFCCHKRRREKEVEVHHIDREVPPKRTISTARSYLSGNH 299
Db 238 GALIGSLVGAIIISVCFARNKAKAKAKER-----NSKTI----- 273

[illegible]

FT	Region	96..100
FT		/note="CVB-binding region (Claim 6)"
FT	Region	122..127
FT		/note="Ad2/5 and CVB binding region (Claim 6)"
XX		
PN	WO9833819-A1.	
XX		
PD	06-AUG-1998.	
XX		
PE	30-JAN-1998;	98WO-US01724.
XX		
PR	30-JAN-1997;	97US-0036986.
XX		
PA	(UYNY) UNIV NEW YORK STATE.	
XX		
PI	Phillipson L, Tomko RP;	
XX		
DR	WPI, 1998-437397/37.	
DR	N-PSDB; AAV50429.	

Claim 3, page 67-68, 80pp; English.

This is the amino acid sequence of human HCAR, a protein that serves as a cellular receptor for adenoviruses of the serotypes 2 and 5 (subgroup C) and for the group B coxsackieviruses (CVB). The sequence was deduced from an isolated cDNA clone for HCAR (see AAV50423). The invention also provides host cells transformed with DNA molecules encoding HCAR or mouse MCR (see AAM69698) and methods of producing the recombinant proteins or their derivatives. These proteins, their extracellular domains, as well as oligopeptides (see AAM69699-708) which bind virus, are claimed. Isolated HCAR or MCR proteins or their fragments or variants are used to prevent or treat virus infections and for inhibiting the infectivity of Ad2, Ad5 or CVB. Methods are also provided for detecting or measuring the quantity of HCAR or MCR in a sample, and for identifying analytes capable of binding to HCAR or MCR.

Sequence 365 AA;

Bay Match	92.48;	Score 1754;	DB 19;	Length 365;
1st Local Similarity	90.78;	Pred. No. 6.9e-150;		
Matches 331; Conservative	16;	Mismatches 18;	Indels 0;	Gaps 0

```

1 MALLCFCVLLCGVADFTSLSTITPEOMIEKAGETAYLPCRFNLGPDQGPLDIEMWLS    60
| | | | | | | | | | | | | | | : | | | | | | | | | |
1 mallcfcvllcgvadftslsttpeomiekargetaylpckrftlspdqgpldiemwls    60
```

61 PADNOKVDVILLYSGDKYDDYDYLKGRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120

61 padnqkvdvqvillysgdkrydyydpdlkgrvhtsndlkskdasinvtndlgdsldtgygc 120
121 kvkkaabvgcnkktotwvlfkpcgtbcvungseetfndnertkcpkccstplfvnqvln 180

```
121 kvkkapgvankihlvtlvkpsgarcyvdgseeisdsfkiacepkegslplqyewqklisd 180
```

181 SÖKPLTWLAEMTSPVIAVKNASTEYSGTYSCTVKNRVGSDDCLLRDVPVPSNRAGTIA 240

```
181 sqkmptswlaemtssvsvknasseysgttysectvrnvgsdqcllrlnvpnsnaglla 240
```

```

241 gaiqgtllalaliglifcrrkkrreekyekvnhdiredvppkstrstarsyignhs 300

```

301 SLGSMSPSMEGYSKTOYNOPSEDFERAPO\$PTLPLAKVAAPNLSRMGAVPVMIPAQ\$K 360

301 slgsmpsnmegysktqynqvpsedfertpqsptlppakvaapnlsrmgaipvmipagsk 360

361 DGSIV 365

Db	361	dgslv	365
	RESULT	2	
	AAW57212		
	AAW57212	standard; Protein; 365	AA.
XX			
XX	AAW57212;		
AC			
XX			
DT	03-AUG-1998	(first entry)	
XX			
DE			
XX	Human coxsackievirus and adenovirus receptor.		
KM	Human: coxsackievirus; adenovirus; receptor; CAR; cardiac infection;		
KW	myocarditis; pericarditis; dilated cardiomyopathy; meningencephalitis		
KW	pancreatic infection; acute pancreatitis; gastrointestinal tract;		
KW	diabetes mellitus.		
XX			
OS	Homo sapiens.		
XX			
XX			
Key		Location/Qualifiers	
FM			
FT	Misc-difference 188		
FT	/note= "encoded by TCG"		

19-MAR-1998.

12-SEP-1997; 97WO-US16189.

13-SEP-1996; 96US-0026100.

(DAND) DANA FARBBER CANCER INST INC.

Bergelson JM, Finberg RW, Horowitz MS;

WPI; 1998-207384/18.

REDD, MARYZOO:

Claim 12, Fig 1B; 104pp; English.

Claim 12; Fig 1B; 104pp; English.

The present sequence represents human coxsackievirus and adenovirus receptor (CAR). The present invention also describes: (1) a method for modulating CAR expression comprising contacting the cell with an agent which modulates CAR protein activity or CAR nucleic acid expression, such that a cell associated activity is altered relative to a cell associated activity of the cell in the absence of the agent; and (2) a method for detecting the presence of CAR in a biological sample comprising contacting a biological sample with an agent capable of detecting CAR protein or mRNA such that the presence of CAR is detected. Modulation of CAR is useful for treatment of cardiac infection, e.g. myocarditis, pericarditis or dilated cardiomyopathy, or infection of the central nervous system, e.g. a non-specific febrile illness or meningoencephalitis, or pancreatic infection, e.g. acute pancreatitis, or infection of the respiratory or gastrointestinal tract or childhood onset diabetes mellitus. Probes derived from CAR nucleic acids are useful for hybridisation assays, and antibodies raised against CAR protein are useful for blocking CAR expression. Cell-free assays which include combining CAR protein and a candidate/test compound are useful in screening for drugs which interact with CAR protein.

Sequence 365 AA;

92.48; Score 1754; DB 19; Length 365;

Matches 331; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

1 MALLCFVLLCGVADLTRSLITPEQMIKAKGETAYLPCRFTLGPEQGPLDIWLLS 60

PI Watanabe CK, Wood WI;
XX
XX WPI: 2001-226690/23.
DR N-PSDB: AAD02924.
XX
XX New PRO polypeptides for treating immune related and inflammatory
PT diseases such as rheumatoid arthritis, systemic vasculitis, asthma,
PT autoimmune hemolytic anemia, and diabetes mellitus
XX
XX
PS Claim 10: Fig 10; 118pp; English.

XX The present sequence is PRO5723 protein encoded by DNA82361 cDNA
CC Clone. PRO protein, its agonist or antagonist or its antibody which are
CC capable of enhancing or inhibiting the proliferation of T-lymphocytes
CC or of increasing the infiltration of inflammatory cells into a tissue
CC are useful in the diagnosis and treatment of immune-related diseases
CC in mammals. The PRO protein is useful for treating systemic lupus
CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
CC arthritis, spondyloarthritis, systemic sclerosis, idiopathic
CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
CC sarcoidosis, autoimmune hemolytic anemia, autoimmune thrombocytopenia,
CC thyroiditis, diabetes mellitus, immune-mediated renal disease,
CC demyelinating disease of the central or peripheral nervous system,
CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC chronic inflammatory demyelinating polyneuropathy, hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, autoimmune or immune-mediated skin diseases such as bullous
CC skin disease, erythema multiforme and contact dermatitis, psoriasis,
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria, immunologic diseases of the lung
CC such as eosinophilic pneumonias, idiopathic pulmonary fibrosis, hyper-
CC sensitivity pneumonitis, transplantation associated diseases such as
CC graft rejection or graft-versus-host-disease.

XX Sequence 352 AA:

Query Match Best Local Similarity 86.0%; Score 1632; DB 22; Length 352;
Matches 307; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTSLSTPTPEQMIKANGETAALPCRFPLGPDGQPLDIEMWLS 60
DB 1 MALLLCFVLLCGVADLTSLSTPTPEQMIKANGETAALPCRFPLGPDGQPLDIEMWLS 60
QY 61 PADNOKVDOYIILYSGDKITDYDYODLKGKRVHFTSNDLKSGDASINTNLQSDIGTYQC 120
DB 61 PADNOKVDOYIILYSGDKITDYDYODLKGKRVHFTSNDLKSGDASINTNLQSDIGTYQC 120
QY 121 KVKRKGVGKIKIQLATPLKPSGTRCYVDGSEETGNDKCEPKESLPLTEMOKLSN 180
DB 121 KVKRKGVGKIKIQLATPLKPSGTRCYVDGSEETGNDKCEPKESLPLTEMOKLSN 180
QY 181 SOKLPTLTLAEMTSPIVSNASTEGTSCYTKNRVSGDOCLLRIDVPPSPRRACTIA 240
DB 181 SOKLPTLTLAEMTSPIVSNASTEGTSCYTKNRVSGDOCLLRIDVPPSPRRACTIA 240
QY 241 GAVIGVLLALVILGLIVCCFKRRREKREYEHHDIREDVPPKSFSTARSATYSGNSH 300
DB 241 GAVIGVLLALVILGLIVCCFKRRREKREYEHHDIREDVPPKSFSTARSATYSGNSH 300
QY 301 SLTSMSPSNMEGYSKTOYNQVPSDFRAPOSPTPLAKVAAP 343
DB 301 SLTSMSPSNMEGYSKTOYNQVPSDFRAPOSPTPLAKVAAP 343
QY 301 SLTSMSPSNMEGYSKTOYNQVPSDFRAPOSPTPLAKVAAP 343
DB 301 SLTSMSPSNMEGYSKTOYNQVPSDFRAPOSPTPLAKVAAP 343

RESULT 6
AAB65294
ID AAB65294 standard; protein; 352 AA.
XX
AC AAB65294;

XX 02-APR-2001 (first entry)
DT Human PRO5723 protein sequence SEQ ID NO:505.
XX
DE Human PRO5723 protein sequence SEQ ID NO:505.
KW Human: secreted and transmembrane protein; PRO; cytosolic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000MO-US08439.
XX
XX 02-JUN-1999; 99MO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99MO-US21090.
PR 15-SEP-1999; 99MO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99MO-US28313.
PR 01-DEC-1999; 99MO-US28301.
PR 16-DEC-1999; 99MO-US30095.
PR 20-DEC-1999; 99MO-US30911.
PR 05-JAN-2000; 2000MO-US00219.
PR 06-JAN-2000; 2000MO-US00376.
PR 11-FEB-2000; 2000MO-US03565.
PR 18-FEB-2000; 2000MO-US04341.
PR 22-FEB-2000; 2000MO-US04414.
PR 24-FEB-2000; 2000MO-US04914.
PR 24-FEB-2000; 2000MO-US05004.
PR 02-MAR-2000; 2000MO-US05841.
PR 15-MAR-2000; 2000MO-US06884.
PR 20-MAR-2000; 2000MO-US07377.
XX
PA (GENT) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kijavain IU, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI: 2001-032160/04.
DR N-PSDB: AAF44263.
XX
XX PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
PS Claim 12: Fig 318; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridization probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridization probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.

```

XX      SQ      Sequence      352 AA:
Query Match      86.0%: Score 1632: DB 22: Length 352:
Best Local Similarity 89.5%: Pred. No. 6.9e-139:
Matches 307: Conservative 15: Mismatches 21: Indels 0: Gaps 0:

OY      1 MALLLCFVLLCGVADLTSLSTITPEOMIEKAKGETAYLPCEFTLGPEDOGPLDIEMILS 60
DB      1 malllcfvllcgvdafarslsitpeemkekagctaylpckftlspedqgpldiemil 60

OY      61 PADNOKVQDVITLLYSGDKTYDDYODLKGRIHFTSNDLKSGASINVTNLQSDIGTYQC 120
DB      61 padnqkvqdvillysgdktyddypdlkgrvhtsndlksagasinvtnlqsdigtqyc 120

OY      121 KYKKA PGVGNKKIQTLLVLLKPGSTGRCYVDSGEISGDFIKCEPKEGSLPILEYEQKLSL 180
DB      121 kykka pygnankihlvllvkpsgarcyvdgseeisgdfikcepegslpiylewqklsd 180

OY      181 SOKLPTLWLAEMTSPVIVSKNASTEYSGTYSCTVKNRVGSDOCLRLDVPSPNRAQTIA 240
DB      181 sqkmlptswlaemtssvsvsknasseysgtysctvrnrvsgdqclrlnvppsnkaglla 240

OY      241 GAVIGVLLALVILGLIVFCCHKKRBEKEKEVHHDIREDVPPPKSRSTANSYLGSNHS 300
DB      241 galigvllalalilglifccrkkrrckkreekvhndiredvpppkststarsyigsns 300

OY      301 SIGSMSPSNMEGYSKTYQVNPSEDEPERAPQPTLLAKVAP 343
DB      301 sigmspsnmeigy sktyqnpsederetpqpcllpakfkyp 343

RESULT 7
ID      AAB50930 standard: Protein: 352 AA.
AC      AAB50930:
DT      21-MAR-2001 (first entry)
DE      Human PRO5723 protein.
XX      Human; PRO: antiinflammatory; dermatological; antiarthritic;
KM      antirheumatic; cardiant; antihaemic; immunosuppressive; antithyroid;
KM      antidiabetic; nootropic; neuroprotective; hepatotopic; virucide;
KM      antiallergic; antiasthmatic; immune related disorder;
KM      hepatobiliary disease; autoimmune disease; allergy.
XX      Homo sapiens.
XX      WO200073452-A2.
XX      07-DEC-2000.
XX      02-JUN-2000: 2000MO-US15264.
XX      02-JUN-1999: 99MO-US12252.
XX      20-JUL-1999: 99US-0144732.
XX      20-JUL-1999: 99US-0144758.
XX      28-JUL-1999: 99US-0146222.
XX      01-SEP-1999: 99MO-US20111.
XX      15-SEP-1999: 99MO-US21090.
XX      15-SEP-1999: 99MO-US21547.
XX      29-OCT-1999: 99US-0162506.
XX      30-NOV-1999: 99MO-US28313.
XX      01-DEC-1999: 99MO-US28634.
XX      09-DEC-1999: 99US-0170262.
XX      20-DEC-1999: 99MO-US30911.
XX      05-JAN-2000: 2000MO-US00219.
XX      06-JAN-2000: 2000MO-US00376.
XX      11-FEB-2000: 2000MO-US03565.
XX      18-FEB-2000: 2000MO-US04341.

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PR      18-FEB-2000: 2000MO-US04342.
PR      22-FEB-2000: 2000MO-US04414.
PR      24-FEB-2000: 2000MO-US04914.
PR      15-MAR-2000: 2000MO-US06884.
PR      20-MAR-2000: 2000MO-US07377.
PR      21-MAR-2000: 2000MO-US07532.
PR      30-MAR-2000: 2000MO-US08439.
PR      17-MAY-2000: 2000MO-US13705.
PR      22-MAY-2000: 2000MO-US14042.
XX      (GETH ) GENENTECH INC.
XX      PA
XX      PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL,
PI      Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tunas D, Watanabe CK;
PI      Wood WI;
XX      WPI: 2001-025253/03.
XX      DR N-PSDB: AAC91489.
XX      PR Thirty three nucleic acids encoding PRO polypeptides which are useful
PR      in the diagnosis and treatment of immune related disorders, e.g.
PR      PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PR      thyroiditis and diabetes mellitus -
XX      PS Claim 58; Fig 56; 218pp; English.
XX      CC The present sequence is one of thirty three novel PRO polypeptides.
XX      CC The PRO polypeptides, anti-PRO antibodies, agonists and
XX      CC antagonists are useful for treating and diagnosing immune related
XX      CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
XX      CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
XX      CC systemic sclerosis, idiopathic chronic inflammatory myopathies, Sjogren's
XX      CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX      CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
XX      CC immune-mediated renal disease, demyelinating diseases of the central
XX      CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
XX      CC demyelinating polynuropathy or Guillain-Barre syndrome, and chronic
XX      CC inflammatory demyelinating polynuropathy), hepatobiliary diseases
XX      CC (such as infectious, autoimmune chronic active hepatitis, primary
XX      CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
XX      CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
XX      CC disease, autoimmune or immune-mediated skin diseases (such as bullous
XX      CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
XX      CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
XX      CC food hypersensitivity and urticaria), immunological diseases of the
XX      CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
XX      CC and hypersensitivity pneumonitis), transplantation associated diseases
XX      CC including graft rejection and graft-versus-host diseases.
XX      SQ Sequence 352 AA:

Query Match      86.0%: Score 1632: DB 22: Length 352:
Best Local Similarity 89.5%: Pred. No. 6.9e-139:
Matches 307: Conservative 15: Mismatches 21: Indels 0: Gaps 0:

OY      1 MALLLCFVLLCGVADLTSLSTITPEOMIEKAKGETAYLPCEFTLGPEDOGPLDIEMILS 60
DB      1 malllcfvllcgvdafarslsitpeemkekagctaylpckftlspedqgpldiemil 60

OY      61 PADNOKVQDVITLLYSGDKTYDDYODLKGRIHFTSNDLKSGASINVTNLQSDIGTYQC 120
DB      61 padnqkvqdvillysgdktyddypdlkgrvhtsndlksagasinvtnlqsdigtqyc 120

OY      121 KYKKA PGVGNKKIQTLLVLLKPGSTGRCYVDSGEISGDFIKCEPKEGSLPILEYEQKLSL 180
DB      121 kykka pygnankihlvllvkpsgarcyvdgseeisgdfikcepegslpiylewqklsd 180

OY      181 SOKLPTLWLAEMTSPVIVSKNASTEYSGTYSCTVKNRVGSDOCLRLDVPSPNRAQTIA 240
DB      181 sqkmlptswlaemtssvsvsknasseysgtysctvrnrvsgdqclrlnvppsnkaglla 240

OY      241 GAVIGVLLALVILGLIVFCCHKKRBEKEKEVHHDIREDVPPPKSRSTANSYLGSNHS 300

```

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Db      241  gailgtlalaiaqlilifccrrkreekyekvhhdiredvppkstrstafaryisnhs 300
QY      301  SLGSMSPSMEGYSKTYNQVPSDEFERAPQSPPLAKAAP 343
        301  slgsmspsmegysktyngvpsedferpqsplpaktkyp 343

RESULT  8
AAW69698
ID      AAW69698 standard; Protein; 352 AA.
XX
AC      AAW69698;
XX
DT      07-DEC-1998 (first entry)
XX
DE      Mouse coxsackievirus and Ad2 and Ad5 receptor MCAR protein.
XX
KW      MCAR; coxsackievirus receptor; CVB; adenovirus; Ad2 receptor;
        Ad5 receptor; mouse; infection; vaccine; therapy.
XX
OS      Mus sp.
XX
FH      Key
        Location/Qualifiers
FT      Domain
        /note= "extracellular immunoglobulin domain"
        155..220
        /note= "extracellular immunoglobulin domain"
FT      Region
        45..52
        /note= "CVB binding region (Claim 6)"
FT      Region
        47..51
        /note= "Ad2/5 and CVB binding region (Claim 6)"
FT      Region
        53..57
        /note= "Ad2/Ad5 binding region (Claim 6)"
FT      Region
        69..73
        /note= "Ad2/Ad5 binding region (Claim 6)"
FT      Region
        72..77
        /note= "Ad2/Ad5 binding region (Claim 6)"
FT      Region
        72..77
        /note= "Ad2/5 and CVB binding region (Claim 6)"
FT      Region
        77..79
        /note= "CVB-binding region (Claim 6)"
FT      Region
        96..100
        /note= "Ad2/Ad5 binding region (Claim 6)"
FT      Region
        122..127
        /note= "CVB-binding region (Claim 6)"
FT      Region
        /note= "Ad2/5 and CVB binding region (Claim 6)"
XX
NN      WO9833819-A1.
XX
J      06-AUG-1998.
XX
PF      30-JAN-1998; 98WO-US01724.
XX
PR      30-JAN-1997; 97US-0036986.
XX
PA      (UYNX ) UNIV NEW YORK STATE.
XX
PI      Phillipson L, Tomko RP;
XX
DR      WPI; 1998-437397/37.
XX
DR      N-PSDB; AAV50430.
XX
PT      DNA encoding human receptor for adenovirus C and coxsackievirus B -
PT      for preventing and treating viral infection and rendering cells
PT      susceptible to transformation by adenoviral vectors in gene therapy
XX
XX      Claim 3; Page 70-71; 88pp; English.
XX
CC      This is the amino acid sequence of mouse MCAR, a protein that
CC      serves as a cellular receptor for adenoviruses of the serotypes 2
CC      and 5 (subgroup C) and for the group B coxsackieviruses (CVB). The
CC      sequence was deduced from an isolated cDNA clone for MCAR (see
CC      AAV50430). The invention also provides host cells transformed with

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CC      DNA molecules encoding MCAR or human HCAR (see AAW69697) and methods
CC      of producing the recombinant proteins or their derivatives. These
CC      proteins, their extracellular domains, as well as oligopeptides
CC      (see AAW69699-708) which bind virus, are claimed. Isolated HCAR or
CC      MCAR proteins or their fragments or variants are used to prevent or
CC      treat virus infections and for inhibiting the infectivity of Ad2,
CC      Ad5 or CVB. Methods are also provided for detecting or measuring
CC      the quantity of HCAR or MCAR in a sample, and for identifying
CC      analytes capable of binding to HCAR or MCAR.
XX
SQ      Sequence 352 AA:
XX
Query Match      85.0%; Score 1613; DB 19; Length 352;
Best Local Similarity 89.7%; Pred. No. 3.6e-137;
Matches 304; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

QY      1  MALLCFVLICGVADLRLRSITTPPEQMIKAKGEGYALPCRFPLGPDGQPLDIEMWLS 60
        1  marllcfvllcgladlrfsglsittppegrlekakgetaylpckftlspedgqpldiemwls 60
Db
QY      61  PADNQKVDQYIILYSGKRTDDYQDLKGRVHFTSNLKSGDASINTNQLSDIGTYQC 120
        61  psdnqkvdyiilysgkrtddyqdlkgrvhtfnsnlksgdasintnqlsdigtqyc 120
Db
QY      121  KVRKAPGVGNKKTIQTLVLPKSPGRVYDSEETGNDFFKLCPEKESGLPLYEMOKLSN 180
        121  kvrkapgvggnkktiolvlpkspgrvydseetgndffklcpekesglplyemoklsn 180
Db
QY      121  kvkkgpvaankkflilvlyvpsgrtcfvdsgeigndfkicpekeslplqfemqklsd 180
        121  kvkkgpvaankkflilvlyvpsgrtcfvdsgeigndfkicpekeslplqfemqklsd 180
QY      181  SOKLPTLMAEMTSPVTSVKNASTESGTYSCVYKNRVSGDCLRLDVVPSNRACITIA 240
        181  soklptlmaemtspvtsvknastesytyscvyknrvsgdclrlldvvpsnracltia 240
Db
QY      241  GAVTGVLLALVILGLVFCCHKKRREKYEKVHNDREVPKPKSTARSYLSGNHS 300
        241  gavgvllalvllglvfcchkkrrrekyekevhnrdrevppkpkstarsylsgnhs 300
Db
QY      241  gavgvllalvllgallfcchrrkreekyekvhhdiredvppkstrstafaryisnhs 300
        241  gavgvllalvllgallfcchrrkreekyekvhhdiredvppkstrstafaryisnhs 300
Db
        301  slgsmspsmegysktyngvpsedferpqsplpaktkyp 339
        301  slgsmspsmegysktyngvpsedferpqsplpaktkyp 339

RESULT  9
AAW82729
ID      AAW82729 standard; Protein; 264 AA.
XX
AC      AAW82729;
XX
DT      29-MAR-1999 (first entry)
XX
DE      Adenovirus PAC7SG2-SCAR protein.
XX
KW      PAC7SG2-SCAR; chimeric protein; adenoviral fibre protein; monomer;
KW      trimerisation domain; affinity; substrate; gene therapy vector;
KW      attachment; interaction assay; infection.
XX
OS      Mastadenovirus.
XX
OS      Synthetic.
XX
PN      WO9854346-A1.
XX
PD      03-DEC-1998.
XX
PF      28-MAY-1998; 98WO-US11024.
XX
PR      16-JAN-1998; 98US-0071668.
XX
PR      28-MAY-1997; 97US-0047849.
XX
PA      (GENV-) GENVEC INC.
XX
PI      Brough DE, Einfeld D, Kovacs I, Lizonova A, Roelivink PW;
XX      Wlckham TJ, Yonehiro G;
XX

```

DR WPI: 1999-059848/05.
DR N-PSDB: AAV72025.
XX
XX New adenoviral fibre trimer with reduced binding to native substrate
PT - useful for, e.g. preparing gene therapy vector with minimal
PT ectopic infection for in vitro applications
XX
XX
PS Example 8; Page 58-59; 103pp; English.
XX
XX This sequence represents a novel adenovirus chimeric protein,
CC PACSG2-SCAR. This protein is used in a method for the construction of
CC novel monomers having an N-terminus of an adenoviral fibre protein and
CC a trimerisation domain. Such monomers have lower affinity for native
CC substrate than the native adenoviral fibre trimer. Cell lines containing
CC such monomers are used (i) to propagate adenovirus for use as gene
CC therapy vectors (for in vitro or in vivo applications), (ii) as reagents
CC for studying adenoviral attachment and infection, and (iii) in
CC receptor-ligand interaction assays. The new viruses produce minimal
CC ectopic infection (they can not infect native host cells) so are safer as
CC vectors and can be engineered for selective targeting to other cells.
CC
Sequence 264 AA:

Query Match 60.2%; Score 1142; DB 20; Length 264;
Best Local Similarity 88.4%; Pred. No. 8.2e-95;
Matches 214; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 1 MALLICEVLLCGVADLTSLSTTPPEOMTERKAGETAYLPCSEFTLGPEDGGLDIEMWLS 60
DB 1 mallelcfvllcgvdarfarslsltppeemlekagetaylpcckflslspedqgpldewlls 60
QY 61 PADNOKVDOVILLYSGDKIYDDYODLKG RVHFTSNDLKSGDASINWNLQSLDSTGYOC 120
DB 61 padnqkvddvillysgdklyddypdlkg rvhftsnlksqdaslnvnlqslsdstgyoc 120
QY 121 KYKKAQVGNKKRIQLTVLKPSTGRCYVDGSEIEGNDRLKCEPKEGSLPLIYEMQKLSN 180
DB 121 kykkapgvgnkkrlhlvllvkpsgarcyvdgseeisdflkcepkegslpllyeqwklsd 180
QY 181 SOKLPTLMLAEMTSPVIVSKNASTESGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
DB 181 sqkmlptswlaemtssvsvsknasseysgtyscctvrnrvgsdqclrlrvvpsnrkagsgs 240
QY 241 GA 242
DB 241 gs 242
QY 1:
DB 1:
SUBT 10
AAW82730
ID AAW82730 standard; Protein; 277 AA.
AC AAW82730;
XX
XX 29-MAR-1999 (first entry)
DT
XX Adenovirus SCAR.RGD protein.
XX
XX SCAR.RGD: chimeric protein; adenoviral fibre protein; monomer;
KM trimerisation domain; affinity; substrate; gene therapy vector;
KM attachment; interaction assay; infection.
XX
XX Mastadenovirus.
OS Synthetic.
XX
XX WO9854346-A1.
XX
XX 03-DEC-1998.
PD
XX 28-MAY-1998; 98WO-US11024.
PF
XX 16-JAN-1998; 98US-0071668.
PR

PR 28-MAY-1997; 97US-0047849.
XX
XX (GENV-) GENVEC INC.
XX
XX Brough DE, Einfeld D, Kovacs I, Lizonova A, Roelvink PW;
PI Wickham TO, Yonehiro G;
XX
XX WPI: 1999-059848/05.
DR N-PSDB: AAV72026.
XX
XX
XX New adenoviral fibre trimer with reduced binding to native substrate
PT - useful for, e.g. preparing gene therapy vector with minimal
PT ectopic infection for in vitro applications
XX
XX
PS Example 8; Page 59-60; 103pp; English.
XX
XX This sequence represents a novel adenovirus chimeric protein, SCAR.RGD.
CC This protein is used in a method for the construction of novel monomers
CC having an N-terminus of an adenoviral fibre protein and a trimerisation
CC domain. Such monomers have lower affinity for native substrate than the
CC native adenoviral fibre trimer. Cell lines containing such monomers are
CC used (i) to propagate adenovirus for use as gene therapy vectors (for in
CC vitro or in vivo applications), (ii) as reagents for studying adenoviral
CC attachment and infection, and (iii) in receptor-ligand interaction
CC assays. The new viruses produce minimal ectopic infection (they can not
CC infect native host cells) so are safer as vectors and can be engineered
CC for selective targeting to other cells.
CC
Sequence 277 AA:

Query Match 60.2%; Score 1142; DB 20; Length 277;
Best Local Similarity 88.4%; Pred. No. 8.8e-95;
Matches 214; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 1 MALLICEVLLCGVADLTSLSTTPPEOMTERKAGETAYLPCSEFTLGPEDGGLDIEMWLS 60
DB 1 mallelcfvllcgvdarfarslsltppeemlekagetaylpcckflslspedqgpldewlls 60
QY 61 PADNOKVDOVILLYSGDKIYDDYODLKG RVHFTSNDLKSGDASINWNLQSLDSTGYOC 120
DB 61 padnqkvddvillysgdklyddypdlkg rvhftsnlksqdaslnvnlqslsdstgyoc 120
QY 121 KYKKAQVGNKKRIQLTVLKPSTGRCYVDGSEIEGNDRLKCEPKEGSLPLIYEMQKLSN 180
DB 121 kykkapgvgnkkrlhlvllvkpsgarcyvdgseeisdflkcepkegslpllyeqwklsd 180
QY 181 SOKLPTLMLAEMTSPVIVSKNASTESGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
DB 181 sqkmlptswlaemtssvsvsknasseysgtyscctvrnrvgsdqclrlrvvpsnrkagsgs 240
QY 241 GA 242
DB 241 gs 242
QY 1:
DB 1:
RESULT 11
AAW82731
ID AAW82731 standard; Protein; 397 AA.
AC AAW82731;
XX
XX 29-MAR-1999 (first entry)
DT
XX Adenovirus PACSG2SCAR.sig chimeric protein.
XX
XX PACSG2SCAR.sigDEL: chimeric protein; adenoviral fibre protein;
KM trimerisation domain; affinity; substrate; gene therapy vector;
KM infection; attachment; interaction assay; vector; monomer.
XX
XX Mastadenovirus.
OS Synthetic.
XX

```

PN MW0854346-AI.
XX 03-DEC-1998.
PD
XX
XX PF 28-MAY-1998; 98WO-US11024.
XX PR 16-JAN-1998; 98US-0071668.
PR 28-MAY-1997; 97US-0047849.
XX
XX (GENV-) GENVEC INC.
PA
XX Brough DE, Einfeld D, Kovessi I, Lizonova A, Roelvjink PM;
PI Wickham TJ, Yonehiro G;
XX
XX MPI: 1999-059848/05.
DR N-PsDB; AAV72027.
XX
XX New adenoviral fibre trimer with reduced binding to native substrate
PT - useful for, e.g. preparing gene therapy vector with minimal
PS ectopic infection for in vitro applications

Example 10; Page 60-62; 103pp; English.

CC This sequence represents a novel adenovirus chimeric protein,
XX PACSGZSCAR.slgDEL. This protein is used in a method for the
CC construction of novel monomers having an N-terminal of an adenoviral
XX fibre protein and a trimerisation domain. Such monomers have lower
CC affinity for native substrate than the native adenoviral fibre trimer.
CC Cell lines containing such monomers are used (1) to propagate adenovirus
CC for use as gene therapy vectors (for in vitro or in vivo applications,
CC (11) as reagents for studying adenoviral attachment and infection, and
CC (111) in receptor-ligand interaction assays. The new viruses produce
CC minimal ectopic infection (they can not infect native host cells) so are
CC safer as vectors and can be engineered for selective targeting to other
XX cells.
XX
SQ Sequence 397 AA:

Query Match 60.2%; Score 1142; DB 20; Length 397;
Best Local Similarity 88.4%; Pred. No.1.5e-94;
Matches 214; Conservative 15; Mismatches 13; Indels 0; Gaps 0.

QY 1 MALLLCFVILICVADLTSLSTTPBQMTERKAGETAYLPCRFYLGPEDQGFLDIEMWLIS 60
Db 1 malllctvlllcvavfarslsiltpeemlekagetaylpckftlispedqgldlewlis 60
QY PADNOKVDQVITLYGSDRIYDDYDLDKGRAFTSNDLSGSPASINVTMLQSLDTGYOC 120
Db padnqkvadvililygsdklyddydpdlkgrviftnslksdaslnvtmqlsdlygyac 120
QY 121 KVKKAPGVGNKKIKQLTVLLKPSGTRCYVDGSEIEIGDNFKLPCKEPEGSLLPLYEMOKISN 180
Db 121 kvkkapgvgnkkikhlvlvltkpsgarcyvdgseieigsdfkikcepegssipldyewklsd 180
QY 181 SOKLEPTLMIAEMTSVIVSKNASTFYSCTGYVNRRVSSDCLRLDLVPVPSNRAGTIA 240
Db 181 sqkmpltsvlaemtssvisvkhasseysgtcltvnrvgsoqclrltlrvvpssnkagsgs 240
QY 241 GA 242
Db 241 gs 242

RESULT 12
AAB85732
ID AAB85732 standard; Protein; 192 AA.
XX
XX AC AAB85732;
XX
DT 29-OCT-2001 (first entry)
XX
DE Rat coxsackieviradenovirus receptor (CAR).

```

XX Sterenzellen; Cocksakie-adenovirus receptor; CAR; liver.
 XX
 XX
 OS Rattus sp.
 XX
 PN JP2001149095-A.
 XX
 PD 05-JUN-2001.
 XX
 PF 24-NOV-1999; 99JP-0333334.
 XX
 PR 24-NOV-1999; 99JP-0333334.
 XX
 XX
 PA (KAGA-) KAGAKU GIYUTSU SHINKO JIGYODAN.
 XX (HIRO-) ZH HIROSHIMAKEN SANGYO GIYUTSU SHINKO KI.
 DR WPI: 2001-499382/55.
 DR N-PSDB: AAH/6081.
 XX
 XX
 PT Recognition of activated state of liver Sterenzellen, useful for
 XX diagnosis of liver disorders -
 XX
 PS Disclosure; Page 5-6; 8pp; Japanese.
 XX
 XX The invention relates to a method of recognition of activated state of
 CC liver Sterenzellen with expressed amount of Cocksakie-adenovirus receptor
 CC (CAR) in a sample containing liver Sterenzellen. A liver disorder can
 CC also be diagnosed by comparing expressed amount of CAR in a sample
 CC containing liver Sterenzellen with that of normal cells. The method
 CC provides a reliable diagnosis of liver disorder with activated liver
 CC Sterenzellen. The present sequence represents a rat CAR.
 XX
 SQ Sequence 192 AA;

	Query Match	Similarity	48.2%	Score 914	DB 22	Length 192
	Best Local	Similarity	89.1%	Pred. No. 2e-74		
Matches 171	Conservative	12	Mismatches	9	Indels	0
					Gaps	0
QY	90	RVHFTSNDLKSGDASINVTNLIQLSDITYOCKYKAPGVGNKKIQLTVLLKPSGRFCYVD	149			
DB	1	rvhftsnvdksgdasinvnvtlqtsditygckvkkkapyamnkfltlvtvpsgrtcfvd	60			
QY	150	GSEELGNDFPKLCEPREGSLPLILEMOKRNSNQKLEPTLMLAEMTSPIVSKNASTRYSGT	209			
DB	61	gsgeigndtrfkcepkgsilpliyewqklsdsqkmpfpwlaemtspsvsvknaassygt	120			
QY	210	YSCCTAKNRVSGDQCLRLDVPVPSNRAGTITACAVIGVLLATLVLLIGLIVCCCHKRREERY	269			
DB	121	yscctlqnrvgssqcmrlridavppsmragtlaagavlgllalalyllgallccckkrreeky	180			
QY	270	EKEVHHDIREDV	281			
DB	181	ekevhhdirdev	192			
RESULT 13						
ABBI0359						
ID	ABBI0359	standard	Protein: 426 AA.			
XX	AC	ABBI0359;				
XX	DT	10-JAN-2002 (first entry)				
XX	DE	Human CDNA SEQ ID NO: 667.				
XX	KM	Human; gene therapy; neural disorder; immune system disorder;				
XX	KM	muscular disorder; reproductive disorder; gastrointestinal disorder;				
XX	KM	pulmonary disorder; cardiovascular disorder; renal disorder;				
XX	OS	proliferative disorder; inflammation.				
XX	XX	Homo sapiens.				

PN W0200154474-A2.
XX
PD 02-AUG-2001.
PF
XX
17-JAN-2001; 2001WO-US01349.
PR 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 24-FEB-2000; 2000US-184664P.
PR 02-MAR-2000; 2000US-186350P.
PR 16-MAR-2000; 2000US-189874P.
PR 17-MAR-2000; 2000US-190076P.
PR 18-APR-2000; 2000US-198123P.
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PR 30-JUN-2000; 2000US-215135P.
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PR 14-AUG-2000; 2000US-225268P.
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PR 14-AUG-2000; 2000US-225447P.
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PR 01-SEP-2000; 2000US-229344P.
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PR 05-JAN-2001; 2001US-259678P.
(HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
XX
PI

DB 172 kegederlpkkrldynhgrvllqllmsysgllycctagneagkescvrtv-tgqyvs 230
 OY 236 ACTIAGAVIGVLLALVLIIGLIVFCCHKRREREKEVEH-HDIREDPKPKSTARSY 294
 DB 231 lgmvagavcglvagallllflwlllrkckeyeeerpeirredaepkarlykpsps 290
 OY 295 LCSNHSLSGSMSPSNMEGSKTOYQYNVPSEDFERAPQSTFLPLA-----KV 340
 DB 291 ssgrsrssrsgssstsrstansasrqlstld--aapqglatqayslvgpevrgsepkkv 348
 OY 341 AAPNLSRMGAVPMIPQSK 360
 DB 349 hnanltkaetlpsmipsqsr 368
 RESULT 15
 AAY41692
 ID AAY41692 standard; Protein; 373 AA.
 XX AAY41692;
 DT 07-DEC-1999 (first entry)
 XX Human PRO 363 protein sequence.
 DE Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX Homo sapiens.
 OS
 XX WO9946281-A2.
 PN 16-SEP-1999.
 XX
 PD 08-MAR-1999; 99WO-US05028.
 XX
 PF 10-MAR-1998; 98US-0077450.
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 PR 28-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wood WJ, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 XX WPI, 1999-551358/46.
 DR N-PSDB; AAZ33941.
 XX
 PT New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders.
 PT
 XX
 PS Claim 12; Fig 24; 530p; English.
 PS
 CC The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated

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